

SEQUENCE LISTING

DT06 Rec'd PCT/PTO 2 5 FEB 2005

<110> Kroger, Burkhard
Zelder, Oskar
Kolpprogge, Corinna
Schroder, Hartwig
Hafner, Stefan

<120> Method for Production by Fermentation of Sulphur-Containing Fine
Chemicals (metF)

<130> 13111-00005-US

<150> PCT/EP 2003/009451

<151> 2003-08-26

<150> DE 102 39 308.7

<151> 2002-08-27

<160> 77

<170> PatentIn version 3.3

<210> 1

<211> 984

<212> DNA

<213> corynebacterium diptheriae

<220>

<221> CDS

<222> (1)..(981)

<223> RDI01260

<400> 1

atg	tct	gca	caa	ccg	cta	cct	gct	gcg	tat	cag	cgc	aca	atc	acc	gat	48
Met	Ser	Ala	Gln	Pro	Leu	Pro	Ala	Ala	Tyr	Gln	Arg	Thr	Ile	Thr	Asp	
1				5					10					15		

gtc	att	tcc	atg	cca	aca	ccg	ggc	cag	gtt	ccg	ttt	tct	gta	gag	ttt	96
Val	Ile	Ser	Met	Pro	Thr	Pro	Gly	Gln	Val	Pro	Phe	Ser	Val	Glu	Phe	
			20					25					30			

atg	ccg	cca	cga	gat	gag	gca	gca	gaa	gag	cga	ctc	tgg	aaa	gcc	gcc	144
Met	Pro	Pro	Arg	Asp	Glu	Ala	Ala	Glu	Glu	Arg	Leu	Trp	Lys	Ala	Ala	
			35				40					45				

gaa	gca	ttt	cac	gac	tta	gga	gcc	tct	ttt	gtc	tcc	gtt	act	tat	ggg	192
Glu	Ala	Phe	His	Asp	Leu	Gly	Ala	Ser	Phe	Val	Ser	Val	Thr	Tyr	Gly	
		50				55				60						

gca	ggc	gga	tct	agc	cgc	gag	cgc	aca	atg	cgt	gtc	gcg	cac	aag	ctt	240
Ala	Gly	Gly	Ser	Ser	Arg	Glu	Arg	Thr	Met	Arg	Val	Ala	His	Lys	Leu	
	65				70				75					80		

tct	cgt	cat	ccg	ttg	acc	acg	ctc	gtt	cat	ctc	acg	ctt	gtg	gaa	cac	288
Ser	Arg	His	Pro	Leu	Thr	Thr	Leu	Val	His	Leu	Thr	Leu	Val	Glu	His	
				85				90						95		

acc	caa	gaa	gaa	tta	gaa	gaa	att	ctg	tgc	act	tat	gcg	tcc	cac	ggg	336
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr	Gln	Glu	Glu	Leu	Glu	Glu	Ile	Leu	Cys	Thr	Tyr	Ala	Ser	His	Gly		
			100				105						110				
tgt	tct	aac	tta	ctt	gcc	tgt	cga	ggc	gat	ccc	cct	ggc	act	gac	ccg	384	
Leu	Ser	Asn	Leu	Leu	Ala	Leu	Arg	Gly	Asp	Pro	Pro	Gly	Thr	Asp	Pro		
			115				120				125						
atg	gct	ccg	tgg	gtc	cct	acc	gca	ggc	ggc	cta	gat	tat	gcc	aaa	gat	432	
Met	Ala	Pro	Trp	Val	Pro	Thr	Ala	Gly	Gly	Leu	Asp	Tyr	Ala	Lys	Asp		
			130				135				140						
tgt	atc	gac	ctc	gtg	cgc	aag	act	gag	cag	acc	tcg	cac	ttt	cag	gta	480	
Leu	Ile	Asp	Leu	Val	Arg	Lys	Thr	Glu	Gln	Thr	Ser	His	Phe	Gln	Val		
145				150						155			160				
gga	att	gct	agt	ttc	cca	gaa	ggg	cac	tac	cga	gcg	cct	agc	att	gag	528	
Gly	Ile	Ala	Ser	Phe	Pro	Glu	Gly	His	Tyr	Arg	Ala	Pro	Ser	Ile	Glu		
			165						170			175					
gcg	gat	acg	caa	ttt	aca	ttg	gaa	aag	ctg	cga	gct	ggc	gca	gag	ttt	576	
Ala	Asp	Thr	Gln	Phe	Thr	Leu	Glu	Lys	Leu	Arg	Ala	Gly	Ala	Glu	Phe		
			180						185			190					
tcg	att	acc	cag	atg	ttt	ttt	gat	gtc	gat	cac	tat	tta	cga	ctg	cga	624	
Ser	Ile	Thr	Gln	Met	Phe	Phe	Asp	Val	Asp	His	Tyr	Leu	Arg	Leu	Arg		
			195						200			205					
gat	cgc	ttg	gtt	aag	gcg	gat	cct	gaa	cat	gga	tca	aag	ccg	atc	atc	672	
Asp	Arg	Leu	Val	Lys	Ala	Asp	Pro	Glu	His	Gly	Ser	Lys	Pro	Ile	Ile		
			210			215						220					
cca	gga	ctt	atg	ccc	att	acc	agc	ttg	agg	tcg	gtt	cgt	agg	cag	atg	720	
Pro	Gly	Leu	Met	Pro	Ile	Thr	Ser	Leu	Arg	Ser	Val	Arg	Arg	Gln	Met		
225				230						235			240				
gaa	tta	gca	ggt	gcc	acc	ttg	cct	aag	gct	tta	gaa	aaa	cgg	ctt	ctc	768	
Glu	Leu	Ala	Gly	Ala	Thr	Leu	Pro	Lys	Ala	Leu	Glu	Lys	Arg	Leu	Leu		
			245						250			255					
gac	gca	gcg	cgc	ggc	gat	gag	gaa	gct	cat	cgc	ggc	gat	att	cgc	aaa	816	
Asp	Ala	Ala	Arg	Gly	Asp	Glu	Glu	Ala	His	Arg	Gly	Asp	Ile	Arg	Lys		
			260			265						270					
gta	gga	atc	gaa	gtc	act	act	gag	atg	gca	cag	cgt	ctt	att	tct	gaa	864	
Val	Gly	Ile	Glu	Val	Thr	Thr	Glu	Met	Ala	Gln	Arg	Leu	Ile	Ser	Glu		
			275			280						285					
ggg	atc	cca	gac	atc	cat	ttc	atg	acc	atg	aat	tat	gtt	cga	gcg	acc	912	
Gly	Ile	Pro	Asp	Ile	His	Phe	Met	Thr	Met	Asn	Tyr	Val	Arg	Ala	Thr		
			290			295			300								
caa	gaa	gta	ctc	cat	aat	ctc	ggc	atg	gcg	ccc	gcg	tgg	gga	aca	cag	960	
Gln	Glu	Val	Leu	His	Asn	Leu	Gly	Met	Ala	Pro	Ala	Trp	Gly	Thr	Gln		
305				310						315			320				
caa	ggc	cac	gac	gct	att	cgc	taa									984	
Gln	Gly	His	Asp	Ala	Ile	Arg											
			325														

<210> 2

<211> 327

<212> PRT

<213> corynebacterium diphteriae

<400> 2

```

Met Ser Ala Gln Pro Leu Pro Ala Ala Tyr Gln Arg Thr Ile Thr Asp
 1             5             10             15

Val Ile Ser Met Pro Thr Pro Gly Gln Val Pro Phe Ser Val Glu Phe
          20             25             30

Met Pro Pro Arg Asp Glu Ala Ala Glu Glu Arg Leu Trp Lys Ala Ala
      35             40             45

Glu Ala Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
 50             55             60

Ala Gly Gly Ser Ser Arg Glu Arg Thr Met Arg Val Ala His Lys Leu
 65             70             75             80

Ser Arg His Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Glu His
          85             90             95

Thr Gln Glu Glu Leu Glu Glu Ile Leu Cys Thr Tyr Ala Ser His Gly
          100             105             110

Leu Ser Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Thr Asp Pro
      115             120             125

Met Ala Pro Trp Val Pro Thr Ala Gly Gly Leu Asp Tyr Ala Lys Asp
      130             135             140

Leu Ile Asp Leu Val Arg Lys Thr Glu Gln Thr Ser His Phe Gln Val
145             150             155             160

Gly Ile Ala Ser Phe Pro Glu Gly His Tyr Arg Ala Pro Ser Ile Glu
          165             170             175

Ala Asp Thr Gln Phe Thr Leu Glu Lys Leu Arg Ala Gly Ala Glu Phe
          180             185             190

Ser Ile Thr Gln Met Phe Phe Asp Val Asp His Tyr Leu Arg Leu Arg
      195             200             205

Asp Arg Leu Val Lys Ala Asp Pro Glu His Gly Ser Lys Pro Ile Ile
      210             215             220

Pro Gly Leu Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Met
      225             230             235             240

Glu Leu Ala Gly Ala Thr Leu Pro Lys Ala Leu Glu Lys Arg Leu Leu
          245             250             255

Asp Ala Ala Arg Gly Asp Glu Glu Ala His Arg Gly Asp Ile Arg Lys
          260             265             270

Val Gly Ile Glu Val Thr Thr Glu Met Ala Gln Arg Leu Ile Ser Glu
      275             280             285

```

Gly Ile Pro Asp Ile His Phe Met Thr Met Asn Tyr Val Arg Ala Thr
 290 295 300

Gln Glu Val Leu His Asn Leu Gly Met Ala Pro Ala Trp Gly Thr Gln
 305 310 315 320

Gln Gly His Asp Ala Ile Arg
 325

<210> 3

<211> 924

<212> DNA

<213> Streptomyces lividans

<220>

<221> CDS

<222> (1)..(921)

<223> RSV00084

<400> 3

atg gcc ctc gga acc gca agc acg agg acg gat cgc gcc cgc acg gtg 48
 Met Ala Leu Gly Thr Ala Ser Thr Arg Thr Asp Arg Ala Arg Thr Val
 1 5 10 15

cgt gac atc ctc gcc acc ggc aag acg acg tac tcg ttc gag ttc tcg 96
 Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser
 20 25 30

gcg ccg aag acg ccc aag ggc gag aag aac ctc tgg agc gcg ctg cgg 144
 Ala Pro Lys Thr Pro Lys Gly Glu Lys Asn Leu Trp Ser Ala Leu Arg
 35 40 45

cgg gtc gag gcc gtg gcc ccg gac ttc gtc tcc gtg acc tac ggc gcc 192
 Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
 50 55 60

ggc ggc tcc acg cgc gcc ggc acg gtc cgc gag acc cag cag atc gtc 240
 Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
 65 70 75 80

gcc gac acc acg ctg acc ccg gtg gcc cac ctc acc gcc gtc gac cac 288
 Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
 85 90 95

tcc gtc gcc gag ctg cgc aac atc atc ggc cag tac gcc gac gcc ggg 336
 Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
 100 105 110

atc cgc aac atg ctg gcc gtg cgc ggc gac ccg ccc ggc gac ccg aac 384
 Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
 115 120 125

gcc gac tgg atc gcg cac ccc gag ggc ctg acc tac gcg gcc gaa ctg 432
 Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
 130 135 140

gtc agg ctc atc aag gag tcg gga gac ttc tgc gtc ggc gtc gcc gcc 480
 Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala
 145 150 155 160

ttc ccc gag atg cac ccg cgc tcc gcc gac tgg gac acg gac gtc acg 528
 Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
 165 170 175

aac ttc gtc gac aag tgc cgg gcc ggc gcc gac tac gcc atc acc cag 576
 Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
 180 185 190

atg ttc ttc cag ccc gac tcc tac ctc cgg ctg cgc gac cgg gtc gcc 624
 Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala
 195 200 205

gcg gcc ggc tgc gcg acc ccg gtc att ccc gag gtc atg ccg gtg acc 672
 Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
 210 215 220

agt gtg aag atg ctg gag agg ttg ccg aag ctc agc aac gcc tcg ttc 720
 Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
 225 230 235 240

ccg gcg gag ctg aaa gag cgg atc ctc aca gcc aag gac gat ccg gcg 768
 Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
 245 250 255

gct gta cgc tcg atc ggc atc gag ttc gcc acg gag ttc tgc gcg cgg 816
 Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
 260 265 270

ctg ctg gcc gag gga gtg cca gga ctg cac ttc atc acg ctc aac aac 864
 Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
 275 280 285

tcc acg gcg acg ctg gaa atc tac gag aac ctg ggc ctg cac cac cca 912
 Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro
 290 295 300

ccg cgg gcc tag 924
 Pro Arg Ala
 305

<210> 4

<211> 307

<212> PRT

<213> Streptomyces lividans

<400> 4

Met Ala Leu Gly Thr Ala Ser Thr Arg Thr Asp Arg Ala Arg Thr Val
 1 5 10 15

Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser
 20 25 30

Ala Pro Lys Thr Pro Lys Gly Glu Lys Asn Leu Trp Ser Ala Leu Arg
 35 40 45

Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
 50 55 60

Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
 65 70 75 80
 Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
 85 90 95
 Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
 100 105 110
 Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
 115 120 125
 Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
 130 135 140
 Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala
 145 150 155 160
 Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
 165 170 175
 Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
 180 185 190
 Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala
 195 200 205
 Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
 210 215 220
 Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
 225 230 235 240
 Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
 245 250- 255
 Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
 260 265 270
 Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
 275 280 285
 Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro
 290 295 300
 Pro Arg Ala
 305

<210> 5
 <211> 924
 <212> DNA
 <213> Streptomyces coelicolor

<220>
 <221> CDS
 <222> (1)..(921)
 <223> RSX01699

<400> 5

atg gcc ctc gga acc gca agc acg agg acg gat cgc gcc cgc acg gtg	48
Met Ala Leu Gly Thr Ala Ser Thr Arg Thr Asp Arg Ala Arg Thr Val	
1 5 10 15	
cg t gac atc ctc gcc acc ggc aag acg acg tac tcg ttc gag ttc tcg	96
Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser	
20 25 30	
gcg ccg aag acg ccc aag ggc gag agg aac ctc tgg agc gcg ctg cgg	144
Ala Pro Lys Thr Pro Lys Gly Glu Arg Asn Leu Trp Ser Ala Leu Arg	
35 40 45	
cgg gtc gag gcc gtg gcc ccg gac ttc gtc tcc gtg acc tac ggc gcc	192
Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala	
50 55 60	
ggc ggc tcc acg cgc gcc ggc acg gtc cgc gag acc cag cag atc gtc	240
Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val	
65 70 75 80	
gcc gac acc acg ctg acc ccg gtg gcc cac ctc acc gcc gtc gac cac	288
Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His	
85 90 95	
tcc gtc gcc gag ctg cgc aac atc atc ggc cag tac gcc gac gcc ggg	336
Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly	
100 105 110	
atc cgc aac atg ctg gcc gtg cgc ggc gac ccg ccc ggc gac ccg aac	384
Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn	
115 120 125	
gcc gac tgg atc gcg cac ccc gag ggc ctg acc tac gcg gcc gaa ctg	432
Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu	
130 135 140	
gtc agg ctc atc aag gag tcg ggc gac ttc tgc gtc ggc gtc gcg gcc	480
Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala	
145 150 155 160	
ttc ccc gag atg cac ccg cgc tcc gcc gac tgg gac acg gac gtc acg	528
Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr	
165 170 175	
aac ttc gtc gac aag tgc cgg gcc ggc gcc gac tac gcc atc acc cag	576
Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln	
180 185 190	
atg ttc ttc cag ccc gac tcc tat ctc cgg ctg cgc gac cgg gtc gcc	624
Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala	
195 200 205	
gcg gcc ggc tgc gcg acc ccg gtc atc ccc gag gtc atg ccg gtg acc	672
Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr	
210 215 220	
agt gtg aag atg ctg gag agg ttg ccg aag ctc agc aac gcc tcg ttc	720
Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe	
225 230 235 240	

ccg gcg gag ttg aaa gag cgg atc ctc aca gcc aag gac gat ccg gcg 768
 Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
 245 250 255

gct gta cgc tcg atc ggc atc gag ttc gcc acg gag ttc tgc gcg cgg 816
 Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
 260 265 270

ctg ctg gcc gag gga gtg cca gga ctg cac ttc atc acg ctc aac aac 864
 Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
 275 280 285

tcc acg gcg acg ctg gaa atc tac gag aac ctg ggc ctg cac cac cca 912
 Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro
 290 295 300

ccg cgg gcc tag 924
 Pro Arg Ala
 305

<210> 6

<211> 307

<212> PRT

<213> Streptomyces coelicolor

<400> 6

Met Ala Leu Gly Thr Ala Ser Thr Arg Thr Asp Arg Ala Arg Thr Val
 1 5 10 15

Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser
 20 25 30

Ala Pro Lys Thr Pro Lys Gly Glu Arg Asn Leu Trp Ser Ala Leu Arg
 35 40 45

Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
 50 55 60

Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
 65 70 75 80

Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
 85 90 95

Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
 100 105 110

Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
 115 120 125

Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
 130 135 140

Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala
 145 150 155 160

Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
 165 170 175

Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
 180 185 190
 Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala
 195 200 205
 Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
 210 215 220
 Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
 225 230 235 240
 Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
 245 250 255
 Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
 260 265 270
 Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
 275 280 285
 Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro
 290 295 300
 Pro Arg Ala
 305

<210> 7
 <211> 891
 <212> DNA
 <213> Aquifex aeolicus

<220> .
 <221> CDS
 <222> (1)..(888)
 <223> RAA00346

<400> 7
 atg aaa ata gga gat ata ctg agg aaa gga gtt ttc agt att tct ttt 48
 Met Lys Ile Gly Asp Ile Leu Arg Lys Gly Val Phe Ser Ile Ser Phe
 1 5 10 15
 gag ttc ttt cca ccg aag act gaa gag gga gaa aga cag ctc ttt gaa 96
 Glu Phe Phe Pro Pro Lys Thr Glu Glu Gly Glu Arg Gln Leu Phe Glu
 20 25 30
 act ata agg aaa ctt gag aaa tta aat cct act ttt gta tcc gtt act 144
 Thr Ile Arg Lys Leu Glu Lys Leu Asn Pro Thr Phe Val Ser Val Thr
 35 40 45
 tac ggg gca ggt ggt tcg act aga gat aga act agg aat ata gta cag 192
 Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Arg Asn Ile Val Gln
 50 55 60
 aaa ata cac gag gaa act aac ctc acc gtt atg gca cac ctc acc tgt 240
 Lys Ile His Glu Glu Thr Asn Leu Thr Val Met Ala His Leu Thr Cys
 65 70 75 80

ata gca cac acg aga gag gag ctt att gat atc ctt caa gat tac aaa	288
Ile Ala His Thr Arg Glu Glu Leu Ile Asp Ile Leu Gln Asp Tyr Lys	
85 90 95	
aac ata ggt ata gag aac att ctc gct ttg agg ggg gac gtt ccg agg	336
Asn Ile Gly Ile Glu Asn Ile Leu Ala Leu Arg Gly Asp Val Pro Arg	
100 105 110	
gac aaa ccg gac tgg aga ccg ccg aag ggt gcg tgc aag tat gca aaa	384
Asp Lys Pro Asp Trp Arg Pro Pro Lys Gly Ala Cys Lys Tyr Ala Lys	
115 120 125	
gag ctc gta gaa ctg atc agg aag gag ttc gga gac tgg ttt tct atc	432
Glu Leu Val Glu Leu Ile Arg Lys Glu Phe Gly Asp Trp Phe Ser Ile	
130 135 140	
gga gtg gct tct tat cct gaa gga cat ccg gaa tca ccg aac ctc gag	480
Gly Val Ala Ser Tyr Pro Glu Gly His Pro Glu Ser Pro Asn Leu Glu	
145 150 155 160	
tgg gaa gtg aag tac ttt aag gaa aag gta gag gca ggt gca gac ttc	528
Trp Glu Val Lys Tyr Phe Lys Glu Lys Val Glu Ala Gly Ala Asp Phe	
165 170 175	
tcg att act cag atg ttt ttc gtg aac gat tac tac tac agg ttt gtg	576
Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val	
180 185 190	
gaa atg tgc aaa aat gca ggg ata gat ata tct ata att ccg gga att	624
Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile	
195 200 205	
atg cct att act aac ttc aaa cag ata aga aag ttt gct tct ctt tgc	672
Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys	
210 215 220	
gga gcg acg att cca cag agt ctt ata gaa aag ctt gaa aaa gtg gag	720
Gly Ala Thr Ile Pro Gln Ser Leu Ile Glu Lys Leu Glu Lys Val Glu	
225 230 235 240	
gat aaa ccg gaa gaa gta aaa aag ata ggg att gag ttt gcc ata aat	768
Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn	
245 250 255	
cag tgt ttg gat ctc ata gaa cac gga gtt ccg ggg ctt cac ttc tac	816
Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr	
260 265 270	
act ctg aac aag tcc gac gca act ttg aag ata tac gag gct ata aag	864
Thr Leu Asn Lys Ser Asp Ala Thr Leu Lys Ile Tyr Glu Ala Ile Lys	
275 280 285	
gat aaa ata ccg gcc cgt tca act taa	891
Asp Lys Ile Pro Ala Arg Ser Thr	
290 295	

<210> 8

<211> 296

<212> PRT

<213> Aquifex aeolicus

<400> 8

```

Met Lys Ile Gly Asp Ile Leu Arg Lys Gly Val Phe Ser Ile Ser Phe
 1             5             10             15

Glu Phe Phe Pro Pro Lys Thr Glu Glu Gly Glu Arg Gln Leu Phe Glu
          20             25             30

Thr Ile Arg Lys Leu Glu Lys Leu Asn Pro Thr Phe Val Ser Val Thr
          35             40             45

Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Arg Asn Ile Val Gln
 50             55             60

Lys Ile His Glu Glu Thr Asn Leu Thr Val Met Ala His Leu Thr Cys
 65             70             75             80

Ile Ala His Thr Arg Glu Glu Leu Ile Asp Ile Leu Gln Asp Tyr Lys
          85             90             95

Asn Ile Gly Ile Glu Asn Ile Leu Ala Leu Arg Gly Asp Val Pro Arg
          100             105             110

Asp Lys Pro Asp Trp Arg Pro Pro Lys Gly Ala Cys Lys Tyr Ala Lys
          115             120             125

Glu Leu Val Glu Leu Ile Arg Lys Glu Phe Gly Asp Trp Phe Ser Ile
          130             135             140

Gly Val Ala Ser Tyr Pro Glu Gly His Pro Glu Ser Pro Asn Leu Glu
          145             150             155             160

Trp Glu Val Lys Tyr Phe Lys Glu Lys Val Glu Ala Gly Ala Asp Phe
          165             170             175

Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val
          180             185             190

Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile
          195             200             205

Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys
          210             215             220

Gly Ala Thr Ile Pro Gln Ser Leu Ile Glu Lys Leu Glu Lys Val Glu
          225             230             235             240

Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn
          245             250             255

Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr
          260             265             270

Thr Leu Asn Lys Ser Asp Ala Thr Leu Lys Ile Tyr Glu Ala Ile Lys
          275             280             285

Asp Lys Ile Pro Ala Arg Ser Thr
          290             295

```

<210> 9
 <211> 831
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS
 <222> (1)..(828)
 <223> RBU14992

<400> 9
 atg aac ccg atc gaa ctt tca ttc gaa ttc ttc ccg ccg aaa acg cag 48
 Met Asn Pro Ile Glu Leu Ser Phe Glu Phe Phe Pro Pro Lys Thr Gln
 1 5 10 15
 gaa ggc gtg gac aag ctg cgc gcc acg cgc gcc cag ctc gcc acg ctc 96
 Glu Gly Val Asp Lys Leu Arg Ala Thr Arg Ala Gln Leu Ala Thr Leu
 20 25 30
 aag ccc aag ttc gtg tcc gtc acg ttc ggc gcc ggc ggc tcg acg caa 144
 Lys Pro Lys Phe Val Ser Val Thr Phe Gly Ala Gly Gly Ser Thr Gln
 35 40 45
 cag ggc acg ctc gac acc gtc gtc gat atg gcg aag gaa ggg ctc gaa 192
 Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu
 50 55 60
 gcg gcg ccg cac gtg tcg tgc atc ggc tcg tcg aaa gag agc ctg cgc 240
 Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg
 65 70 75 80
 gcc att ctc aac gag tac cgc gca cat ggc atc cgc cat atc gtc gcg 288
 Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala
 85 90 95
 ctg cgc ggc gat ctg ccg tcc ggc atg ggc gaa gtc ggc gag ctg cgc 336
 Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg
 100 105 110
 tat gcg tcg gaa ctg gtg agc ttt atc cgc gcc gaa ttc ggc gac tgg 384
 Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp
 115 120 125
 ttc tgc atc gag gtg gcc ggc tat ccg gaa tac cac ccg cag tcg cgc 432
 Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg
 130 135 140
 tcg ccg cgt cag gat ctg gaa aac ttc gcc cgc aag gtg aag gcc ggc 480
 Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly
 145 150 155 160
 gcc aat tcg gcg atc aca cag tac ttc ttc aat gca gac gcg tat ttc 528
 Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe
 165 170 175
 cgt ttc gtc gac gac gcg aga aag ctc ggc gtg gac gtg ccg atc gtg 576
 Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val

180	185	190	
ccg ggc atc atg ccg atc acg aac ttc tcg cag ctg atg cgt ttc tcg			624
Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser			
195	200	205	
gag atg tgc ggc gct gaa gtg cca cgc tgg atc gcg cgc cgg ctg gaa			672
Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu			
210	215	220	
agc ttc ggc gac gat cgc gag tca att cgc gcg ttc ggg ctg gat gtg			720
Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val			
225	230	235	240
gtg acg gac ctg tgc agg cgt ctg atc gat gcg aag gtg ccg ggc ctg			768
Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu			
	245	250	255
cac ttc tac acg cta aac ggc gca gcg gcg acc aag gcg atc tgc gaa			816
His Phe Tyr Thr Leu Asn Gly Ala Ala Thr Lys Ala Ile Cys Glu			
	260	265	270
cgg ttg aac gtt taa			831
Arg Leu Asn Val			
275			

<210> 10
 <211> 276
 <212> PRT
 <213> Burkholderia cepacia

<400> 10
 Met Asn Pro Ile Glu Leu Ser Phe Glu Phe Phe Pro Pro Lys Thr Gln
 1 5 10 15
 Glu Gly Val Asp Lys Leu Arg Ala Thr Arg Ala Gln Leu Ala Thr Leu
 20 25 30
 Lys Pro Lys Phe Val Ser Val Thr Phe Gly Ala Gly Gly Ser Thr Gln
 35 40 45
 Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu
 50 55 60
 Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg
 65 70 75 80
 Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala
 85 90 95
 Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg
 100 105 110
 Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp
 115 120 125
 Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg
 130 135 140

Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly
 145 150 155 160
 Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe
 165 170 175
 Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val
 180 185 190
 Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser
 195 200 205
 Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu
 210 215 220
 Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val
 225 230 235 240
 Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu
 245 250 255
 His Phe Tyr Thr Leu Asn Gly Ala Ala Ala Thr Lys Ala Ile Cys Glu
 260 265 270
 Arg Leu Asn Val
 275

<210> 11
 <211> 846
 <212> DNA
 <213> Nitrosomonas europaea

<220> .
 <221> CDS
 <222> (1)..(843)
 <223> RNE02657

<400> 11

atg caa tcc cag aaa aaa ttt acc ccc aca ttc agt ttt gaa ttt ttc 48
 Met Gln Ser Gln Lys Lys Phe Thr Pro Thr Phe Ser Phe Glu Phe Phe
 1 5 10 15
 ccg ccg cag aca ccg gaa ggc atg gaa aag ctg cgg gca acg cgc ata 96
 Pro Pro Gln Thr Pro Glu Gly Met Glu Lys Leu Arg Ala Thr Arg Ile
 20 25 30
 cag ctt gct cag ttc aat ccg aag ttt ttt tcg gtg acg ttt ggt gcc 144
 Gln Leu Ala Gln Phe Asn Pro Lys Phe Phe Ser Val Thr Phe Gly Ala
 35 40 45
 ggc gga tcc act cgt gaa cgc acg ctc gaa acc gtg ctg gaa att cag 192
 Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln
 50 55 60
 gca gaa ggc tat ccg gta gcg ccc cat ctt tcc tgt atc ggc tcc acg 240
 Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr
 65 70 75 80

cgt gac aat atc cgt tgc atc ctt gag aaa tat cac agt cac ggt atc	288
Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile	
85 90 95	
agc cgc att gtg gcg cta cgt ggt gat tta ccc tcc ggc atg gcg cag	336
Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln	
100 105 110	
gcg gga gaa ttc cgc tac gcc aac gag ctg gta gca ttt atc cgc aag	384
Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys	
115 120 125	
gag ttc ggt gat acc ttc tgg atc gaa gtg gcg gct tat ccg gaa tat	432
Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr	
130 135 140	
cat cca caa gcc cgc tcc gct ctg gag gat ttc acc aat ttc aga cga	480
His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg	
145 150 155 160	
aaa gtc gaa gca ggt tcc aat gca gcg att acc cag ttt ttc tat aac	528
Lys Val Glu Ala Gly Ser Asn Ala Ala Ile Thr Gln Phe Phe Tyr Asn	
165 170 175	
gtg gat gcc tat ctg cat ttc gta gag atg tgt gaa gct gcg gat ctg	576
Val Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu	
180 185 190	
aat atc ccg atc gtt ccc ggc atc atg ccg atc agc aaa ttt tct caa	624
Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln	
195 200 205	
ctg gca aga ttt tgc gat ggc tgt gga gca gaa att cca cgc tgg att	672
Leu Ala Arg Phe Ser Asp Gly Cys Gly Ala Glu Ile Pro Arg Trp Ile	
210 215 220	
cgc aga aaa ctg gaa agc ttc ggt gat gat att ccg tct atc cag gca	720
Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala	
225 230 235 240	
ttc ggg ctg gat gtc gtc aca gcg tta tgt gct cgt ctg ctg gaa gcc	768
Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala	
245 250 255	
ggc gca ccc ggc ctg cat ttc tac aca ctc aac tcc gcc gta cta ccc	816
Gly Ala Pro Gly Leu His Phe Tyr Thr Leu Asn Ser Ala Val Leu Pro	
260 265 270	
aca aaa atc tgg caa cgc ctg ggg tta tag	846
Thr Lys Ile Trp Gln Arg Leu Gly Leu	
275 280	

<210> 12

<211> 281

<212> PRT

<213> Nitrosomonas europaea

<400> 12

Met Gln Ser Gln Lys Lys Phe Thr Pro Thr Phe Ser Phe Glu Phe Phe
 1 5 10 15
 Pro Pro Gln Thr Pro Glu Gly Met Glu Lys Leu Arg Ala Thr Arg Ile
 20 25 30
 Gln Leu Ala Gln Phe Asn Pro Lys Phe Phe Ser Val Thr Phe Gly Ala
 35 40 45
 Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln
 50 55 60
 Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr
 65 70 75 80
 Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile
 85 90 95
 Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln
 100 105 110
 Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys
 115 120 125
 Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr
 130 135 140
 His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg
 145 150 155 160
 Lys Val Glu Ala Gly Ser Asn Ala Ala Ile Thr Gln Phe Phe Tyr Asn
 165 170 175
 Val Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu
 180 185 190
 Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln
 195 200 205
 Leu Ala Arg Phe Ser Asp Gly Cys Gly Ala Glu Ile Pro Arg Trp Ile
 210 215 220
 Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala
 225 230 235 240
 Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala
 245 250 255
 Gly Ala Pro Gly Leu His Phe Tyr Thr Leu Asn Ser Ala Val Leu Pro
 260 265 270
 Thr Lys Ile Trp Gln Arg Leu Gly Leu
 275 280

<210> 13

<211> 873

<212> DNA

<213> *Pseudomonas aeruginosa*

<220>

<221> CDS

<222> (1)..(870)

<223> RPA03308

<400> 13

gtg gtc gcg tcc aag gaa ccg atc atg agt cag agc gaa cgc cgt ttc	48
Val Val Ala Ser Lys Glu Pro Ile Met Ser Gln Ser Glu Arg Arg Phe	
1 5 10 15	
agc ttc gag ttc ttc ccg gcg aag acc gag gcc ggc cat gaa aag ctg	96
Ser Phe Glu Phe Phe Pro Ala Lys Thr Glu Ala Gly His Glu Lys Leu	
20 25 30	
ttg gcc acc gcc cgc aac ctg gcg ggc tac aag ccc gac ttc ttc tcc	144
Leu Ala Thr Ala Arg Asn Leu Ala Gly Tyr Lys Pro Asp Phe Phe Ser	
35 40 45	
tgc acc tac ggc gcc ggc gga tcc acc cgc gac cgc acg ttg agt acc	192
Cys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr	
50 55 60	
gtg ctg caa ctg gac ggc gag gtg aag gtg ccg acc gcg ccg cac ctg	240
Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu	
65 70 75 80	
tcc tgt gtc ggc gac tcg aaa gcc gag ttg cgc gaa ctg ctc ggc cgc	288
Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg	
85 90 95	
tac cgc gag gcc ggc atc cgc cgc atc gtc gcc ctg cgc ggc gac ctg	336
Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu	
100 105 110	
ccg tcg ggc atg ggc atg gcc agc ggc gaa ctg cgc tac gcc aac gaa	384
Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu	
115 120 125	
ctg gtg gac ttc atc cgc acc gag acc ggc gac cac ttc cac atc gag	432
Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu	
130 135 140	
gtc gcc gcc tat ccg gag gtc cac ccc cag gcg cgc agc ttc gag gat	480
Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp	
145 150 155 160	
gac ctg gcg aac ttc gtg cgc aag gtg aag gcc ggc gcc agc agc gcc	528
Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala	
165 170 175	
atc acc cag tac ttc ttc aac gcc gat gcc tat ttc tac ttc gtc gag	576
Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu	
180 185 190	
cgg gtc gcc aag ctg ggc gtg gac atc ccg gtg gtc ccc ggc atc atg	624
Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met	
195 200 205	
ccg atc acc aac tac tcc aag ctg gcg cgc ttc tcc gac gcc tgc ggc	672

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly
 210 215 220

gcc gaa ctg ccg cgc tgg atc cgc aag caa ctg gaa gcc tac ggc gac 720
 Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp
 225 230 235 240

gac agc cgc agc atc cag gcc ttc ggc gag cag gtc atc agc gag atg 768
 Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met
 245 250 255

tgc gaa cgc ctg ctg gag ggc ggc gca ccg gga ctg cat ttc tat act 816
 Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr
 260 265 270

ttg aac cag gcc gat ccg agc ctg gcg atc tgg aag aat ctc cag ctg 864
 Leu Asn Gln Ala Asp Pro Ser Leu Ala Ile Trp Lys Asn Leu Gln Leu
 275 280 285

cca cgc tga 873
 Pro Arg
 290

<210> 14
 <211> 290
 <212> PRT
 <213> Pseudomonas aeruginosa

<400> 14
 Val Val Ala Ser Lys Glu Pro Ile Met Ser Gln Ser Glu Arg Arg Phe
 1 5 10 15

Ser Phe Glu Phe Phe Pro Ala Lys Thr Glu Ala Gly His Glu Lys Leu
 20 25 30

Leu Ala Thr Ala Arg Asn Leu Ala Gly Tyr Lys Pro Asp Phe Phe Ser
 35 40 45

Cys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr
 50 55 60

Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu
 65 70 75 80

Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg
 85 90 95

Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu
 100 105 110

Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu
 115 120 125

Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu
 130 135 140

Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp
 145 150 155 160

Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala
 165 170 175

Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu
 180 185 190

Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met
 195 200 205

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly
 210 215 220

Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp
 225 230 235 240

Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met
 245 250 255

Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr
 260 265 270

Leu Asn Gln Ala Asp Pro Ser Leu Ala Ile Trp Lys Asn Leu Gln Leu
 275 280 285

Pro Arg
 290

<210> 15
 <211> 828
 <212> DNA
 <213> Xylella almond

<220>
 <221> CDS
 <222> (1)..(825)
 <223> RXFX00359

<400> 15
 atg att cca atc agc ttc gag ttt tat cca ccc aaa aac gac gat caa 48
 Met Ile Pro Ile Ser Phe Glu Phe Tyr Pro Pro Lys Asn Asp Asp Gln
 1 5 10 15
 cgc gca cag ttg gac agg aca gca aac cgg cta cgc gca ttc gca cca 96
 Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro
 20 25 30
 gaa tac gtc tcc tgc acc ttc ggc gcc ggt ggc tcc aca ctc agt tac 144
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45
 acc tca gaa aca gtg cgc cat ctc agc caa cac cac ggc ttt gac gcc 192
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala
 50 55 60
 gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa 240
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80

ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta	288
Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu	
85 90 95	
cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac	336
Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	
gca gct gac ctg att acc ttc atc cgt acc gag cat ggc gat cac ttc	384
Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe	
115 120 125	
cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac	432
His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	
aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc	480
Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	
gat gcg gca atc act caa tac ttt tat aac cca gac gcc tat ttc cac	528
Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	
ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc	576
Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
180 185 190	
gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa	624
Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
195 200 205	
caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct	672
Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala	
210 215 220	
tac ggc gac gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg	720
Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val	
225 230 235 240	
acc gca tta tgt gag cgg cta atc gct ggc ggc gca ccg ggg ctg cac	768
Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His	
245 250 255	
ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc	816
Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg	
260 265 270	
tta ggc tat tga	828
Leu Gly Tyr	
275	

<210> 16

<211> 275

<212> PRT

<213> Xylella almond

<400> 16

Met Ile Pro Ile Ser Phe Glu Phe Tyr Pro Pro Lys Asn Asp Asp Gln
 1 5 10 15
 Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro
 20 25 30
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala
 50 55 60
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80
 Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95
 Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
 100 105 110
 Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe
 115 120 125
 His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
 130 135 140
 Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
 145 150 155 160
 Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His
 165 170 175
 Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala
 180 185 190
 Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu
 195 200 205
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
 210 215 220
 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
 225 230 235 240
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
 245 250 255
 Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
 260 265 270
 Leu Gly Tyr
 275

<210> 17

<211> 828

<212> DNA

<213> Xylella oleander

<220>

<221> CDS

<222> (1)..(825)

<223> RXYF01676

<400> 17

atg att cca atc agc ttc gag ttt tat cca ccc aaa aac gac gat caa	48
Met Ile Pro Ile Ser Phe Glu Phe Tyr Pro Pro Lys Asn Asp Asp Gln	
1 5 10 15	
cgc gca cag ttg gac agg aca gca aac cgg cta cgc gca ttc gca cca	96
Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro	
20 25 30	
gaa tac gtc tcc tgc acc ttc ggc gcc ggc ggc tcc aca ctc agt tac	144
Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr	
35 40 45	
acc tca gaa aca gtg cgc cat ctc agt caa cac cac ggc ttt gac acc	192
Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr	
50 55 60	
gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa	240
Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu	
65 70 75 80	
ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta	288
Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu	
85 90 95	
cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac	336
Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	
gca gct gac ctg att acc ttc atc cgt gcc gag cat ggc gat cac ttc	384
Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe	
115 120 125	
cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac	432
His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	
aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc	480
Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	
gat gcg gca atc act caa tac ttt tac aac cca gac gcc tat ttc cac	528
Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	
ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc	576
Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
180 185 190	
gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa	624
Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
195 200 205	

caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct 672
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
 210 215 220

tac ggc gat gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg 720
 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
 225 230 235 240

acc gca cta tgt gag cgg cta atc gct ggc ggc gca ccg ggg ctg cac 768
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
 245 250 255

ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc 816
 Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
 260 265 270

tta ggc tat tga 828
 Leu Gly Tyr
 275

<210> 18
 <211> 275
 <212> PRT
 <213> Xylella oleander

<400> 18
 Met Ile Pro Ile Ser Phe Glu Phe Tyr Pro Pro Lys Asn Asp Asp Gln
 1 5 10 15

Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro
 20 25 30

Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45

Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr
 50 55 60

Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80

Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95

Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
 100 105 110

Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe
 115 120 125

His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
 130 135 140

Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
 145 150 155 160

Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His

	165		170		175
Phe Val Asp	Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala				
	180		185		190
Gly Val Met	Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu				
	195		200		205
Gln Cys Gly	Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala				
	210		215		220
Tyr Gly Asp	Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val				
	225		230		235
Thr Ala Leu	Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His				
	245		250		255
Phe Tyr Thr	Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg				
	260		265		270
Leu Gly Tyr					
	275				

<210> 19

<211> 846

<212> DNA

<213> *Pseudomonas fluorescens*

<220>

<221> CDS

<222> (1)..(843)

<223> RPU04845

<400> 19

atg tcc caa gac cgt cgc tac agc ttc gag ttc ttc ccg acc aag acc	48
Met Ser Gln Asp Arg Arg Tyr Ser Phe Glu Phe Phe Pro Thr Lys Thr	
1 5 10 15	
gat gct ggg cat gaa aaa ctg ctc gcc act gcc cgt cag ctg gcc acc	96
Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr	
20 25 30	
tat aag cct gac ttc ttt tcc tgc acc tac ggc gct ggc ggt tcg acc	144
Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr	
35 40 45	
cgt gac cgc acg ctg aac acc gtt ctg cag ctg gaa agc gaa gtc aaa	192
Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys	
50 55 60	
atc ccc gcc gca ccg cac ctg tcg tgc gtc ggc gac agc aag gac gac	240
Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp	
65 70 75 80	
ctg cgc ggc ctg ctg aac gag tac aag gcc gcc ggc atc aag cgc atc	288
Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile	
85 90 95	

gtc gcc ctg cgc ggt gac ctg ccg tcc ggc atg ggc atg acc agc ggc 336
 Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly
 100 105 110

gag ctg cgt cac gcc aat gaa ctg gtt gaa ttc att cgt gaa gaa acc 384
 Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr
 115 120 125

ggc aat cat ttc cac atc gaa gtc gcc gcc tac ccg gag atg cat ccg 432
 Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro
 130 135 140

caa gcg cgc aac tac gaa gac gat ctc gcc aac ttc gtg cgc aag gcc 480
 Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala
 145 150 155 160

cgt gcc ggc gcc gac agc gcg atc acc cag tac ttc ttc aac gcc gac 528
 Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp
 165 170 175

agc tac ttc tac ttc gtc gac cgt ttg cag gcg ctg ggc gtg gac att 576
 Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile
 180 185 190

ccg gtg gta ccg ggg atc atg ccg atc acc aac tac agc aaa ctc gcg 624
 Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala
 195 200 205

cgc ttc tcc gat gcc tgc ggt gcg gaa atc ccg cgc tgg atc cgc aag 672
 Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys
 210 215 220

cag ctg gaa gcc tac ggc gat gac agc caa agc att cag cgc ttt ggc 720
 Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly
 225 230 235 240

gaa caa gtc gtc acg gaa atg tgc gaa cgc ctg ctg caa ggc ggc gcg 768
 Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala
 245 250 255

ccc ggc ctg cac ttc tat tcc atg aac cag gcc gaa cca agc ctg gcg 816
 Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala
 260 265 270

atc tgg aac aac ctg aag ctg ccg cgc taa 846
 Ile Trp Asn Asn Leu Lys Leu Pro Arg
 275 280

<210> 20

<211> 281

<212> PRT

<213> *Pseudomonas fluorescens*

<400> 20

Met Ser Gln Asp Arg Arg Tyr Ser Phe Glu Phe Phe Pro Thr Lys Thr
 1 5 10 15

Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr
 20 25 30

Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr
 35 40 45
 Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys
 50 55 60
 Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp
 65 70 75 80
 Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile
 85 90 95
 Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly
 100 105 110
 Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr
 115 120 125
 Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro
 130 135 140
 Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala
 145 150 155 160
 Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp
 165 170 175
 Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile
 180 185 190
 Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala
 195 200 205
 Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys
 210 215 220
 Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly
 225 230 235 240
 Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala
 245 250 255
 Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala
 260 265 270
 Ile Trp Asn Asn Leu Lys Leu Pro Arg
 275 280

<210> 21

<211> 1812

<212> DNA

<213> Schizosaccharomyces pombe

<220>

<221> CDS

<222> (1)..(1809)

<223> RSO01645

<400> 21

atg aaa ata agt gac aaa tta ctt cac ccg gat tgg aag gaa aaa gtt	48
Met Lys Ile Ser Asp Lys Leu Leu His Pro Asp Trp Lys Glu Lys Val	
1 5 10 15	
act tac agt tat gaa ttt ttt cct cca aaa acg agc act ggt gtc caa	96
Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln	
20 25 30	
aat ctt tac aat cgt ata gat cgc atg aag act tgg ggt cgt ccc atg	144
Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met	
35 40 45	
ttt gtc gat gtg act tgg ggt gct ggt ggt act tct tca gaa ctg act	192
Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr	
50 55 60	
cct gga atc gtt aat gta att caa aca gat ttt gaa gtg gat act tgc	240
Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys	
65 70 75 80	
atg cat ttg act tgt acg aac atg tcc aca gaa atg att gac gca gct	288
Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala	
85 90 95	
ttg aaa cgg gct cat gaa aca ggg tgt cgt aac ata ttg gcc ctt aga	336
Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg	
100 105 110	
ggg gat cct gtt aaa gat aca gac tgg act gaa ggc gaa agt gga ttc	384
Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe	
115 120 125	
cgg tat gct tca gac tta gtt aga tat att cgc aca cat tat aat gat	432
Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp	
130 135 140	
gaa ttc tgt att ggt gta gct ggc tat cca gaa gga tat tca cca gat	480
Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp	
145 150 155 160	
gat gac att gat gaa agc ata aag cat ctg aaa tta aaa gtc gat gaa	528
Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu	
165 170 175	
ggg gct gat ttt atc gtt act caa atg ttt tat gat gta gac aat ttt	576
Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe	
180 185 190	
atc gca tgg gtc gat aaa gtg cgt gca gca gga ata aat atc cct ata	624
Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile	
195 200 205	
ttt ccg ggc att atg cct att cag gca tgg gat tcc ttt att cgg aga	672
Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg	
210 215 220	
gcg aaa tgg agc ggt gtt aaa att ccc cag cat ttt atg gat act cta	720
Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu	
225 230 235 240	

gtc cca gtt aaa gac gat gat gaa gga gtc cgt gag cgt ggt gtt gag	768
Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu	
245 250 255	
ctc ata gtc gaa atg tgc cgt aag ctt ata gct agt ggc att acg aga	816
Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg	
260 265 270	
ctt cat ttt tac act atg aat tta gaa aag gcc gtt aaa atg att att	864
Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile	
275 280 285	
gaa cga tta ggt tta tta gat gaa aac ttg gct cct ata gtg gat act	912
Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr	
290 295 300	
aat aac gtc gag tta acc aat gct tcc agt caa gat cgt cgg ata aat	960
Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn	
305 310 315 320	
gaa ggt gta cgg ccc att ttc tgg cgc act cgt aat gaa agt tat gtc	1008
Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val	
325 330 335	
tcg cgt act gat cag tgg gac gaa tta ccg cat ggt cgt tgg ggt gac	1056
Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp	
340 345 350	
tct cgt agc cct gct ttt ggc gaa ttt gat gct att aga tat ggt ctt	1104
Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu	
355 360 365	
cgt atg tct ccc aag gag atc aca aca tcg tgg ggg tct cct aaa tct	1152
Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser	
370 375 380	
tac tcg gaa atc ggc gat ttg ttt gcc agg tac tgt gaa aaa aag att	1200
Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile	
385 390 395 400	
agc tcc ctc cct tgg agt gat ctt ccc ata tcc gat gaa gcc gac ttg	1248
Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu	
405 410 415	
att cgg gat caa ctt cta agt atg aat aga aac gct ttc ctt act ata	1296
Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile	
420 425 430	
aat tct caa cct gct ctt aac ggc gaa aag agt tca cat cct gtt ttt	1344
Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe	
435 440 445	
gga tgg gga cca cct aat ggt tat gtt ttc caa aaa cca tac gtt gag	1392
Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu	
450 455 460	
ttt ttc gtt cac ccc tca ctc ttg aat gaa ctc aaa gaa acc gtt aaa	1440
Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys	
465 470 475 480	

aag ctt aat tca gtt tcc tac ttt gtt aca aac aag aat gga gac ttg 1488
 Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu
 485 490 495

gat acc aac tca caa tat gag att cca aat gcg gtt aca tgg ggt gtt 1536
 Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val
 500 505 510

ttc cct aat cgt gag att atc caa cct act att gtc gag tca acc tct 1584
 Phe Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser
 515 520 525

ttt ctt gct tgg aaa gat gaa gcc tat tca ttg ggc atg gaa tgg gct 1632
 Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala
 530 535 540

aat gca tat agc cct gat tca att tct cgt aaa ctt ttg gtt tct atg 1680
 Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met
 545 550 555 560

atg aag gaa tgg ttc ctt tgt gtc ata gtt gat aac gat ttt caa aat 1728
 Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn
 565 570 575

ggg caa tct ttg ttt gat gtt ttt aac aaa atg aga tct tta aaa gac 1776
 Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp
 580 585 590

atc cat cct gag cta tat tat gca aat gca tca taa 1812
 Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser
 595 600

<210> 22

<211> 603

<212> PRT

<213> Schizosaccharomyces pombe

<400> 22

Met Lys Ile Ser Asp Lys Leu Leu His Pro Asp Trp Lys Glu Lys Val
 1 5 10 15

Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln
 20 25 30

Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met
 35 40 45

Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr
 50 55 60

Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys
 65 70 75 80

Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala
 85 90 95

Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg
 100 105 110

Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe
 115 120 125
 Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp
 130 135 140
 Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp
 145 150 155 160
 Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu
 165 170 175
 Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe
 180 185 190
 Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile
 195 200 205
 Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg
 210 215 220
 Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu
 225 230 235 240
 Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu
 245 250 255
 Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg
 260 265 270
 Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile
 275 280 285
 Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr
 290 295 300
 Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn
 305 310 315 320
 Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val
 325 330 335
 Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp
 340 345 350
 Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu
 355 360 365
 Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser
 370 375 380
 Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile
 385 390 395 400
 Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu
 405 410 415
 Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile
 420 425 430

Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe
435 440 445

Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu
450 455 460

Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys
465 470 475 480

Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu
485 490 495

Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val
500 505 510

Phe Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser
515 520 525

Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala
530 535 540

Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met
545 550 555 560

Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn
565 570 575

Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp
580 585 590

Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser
595 600

<210> 23

<211> 1800

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1797)

<223> RSC08323

<400> 23

atg aag atc aca gaa aaa tta gag caa cat aga cag acc tct ggc aag 48
Met Lys Ile Thr Glu Lys Leu Glu Gln His Arg Gln Thr Ser Gly Lys
1 5 10 15

ccc act tac tca ttc gag tac ttc gtc ccg aag act aca caa ggt gta 96
Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val
20 25 30

cag aac ctg tat gac cgg atg gac cgg atg tac gag gct tct ttg ccc 144
Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro
35 40 45

caa ttt att gac atc acc tgg aat gca ggc ggt gga cgg ttg tca cat 192

Gln	Phe	Ile	Asp	Ile	Thr	Trp	Asn	Ala	Gly	Gly	Gly	Arg	Leu	Ser	His		
50						55					60						
ctg	tcc	acg	gac	ttg	gtt	gcg	aca	gcg	cag	tct	gtg	ctt	ggt	ttg	gaa	240	
Leu	Ser	Thr	Asp	Leu	Val	Ala	Thr	Ala	Gln	Ser	Val	Leu	Gly	Leu	Glu		
65					70					75					80		
acg	tgc	atg	cac	ctt	acc	tgc	acc	aat	atg	ccc	att	tcg	atg	att	gac	288	
Thr	Cys	Met	His	Leu	Thr	Cys	Thr	Asn	Met	Pro	Ile	Ser	Met	Ile	Asp		
				85					90					95			
gac	gct	tta	gaa	aac	gct	tat	cac	tcc	ggt	tgc	cag	aac	atc	cta	gcg	336	
Asp	Ala	Leu	Glu	Asn	Ala	Tyr	His	Ser	Gly	Cys	Gln	Asn	Ile	Leu	Ala		
			100					105					110				
ctg	aga	gga	gat	cct	cct	agg	gac	gca	gaa	aac	tgg	act	ccc	gtt	gaa	384	
Leu	Arg	Gly	Asp	Pro	Pro	Arg	Asp	Ala	Glu	Asn	Trp	Thr	Pro	Val	Glu		
		115					120					125					
ggt	ggc	ttc	cag	tat	gcc	aag	gac	ttg	att	aag	tat	atc	aag	tcc	aag	432	
Gly	Gly	Phe	Gln	Tyr	Ala	Lys	Asp	Leu	Ile	Lys	Tyr	Ile	Lys	Ser	Lys		
	130					135					140						
tac	ggt	gac	cat	ttc	gct	atc	ggc	gtt	gcc	ggc	tac	ccg	gag	tgc	cat	480	
Tyr	Gly	Asp	His	Phe	Ala	Ile	Gly	Val	Ala	Gly	Tyr	Pro	Glu	Cys	His		
145					150					155					160		
ccg	gag	ttg	cct	aac	aaa	gac	gtg	aag	ctt	gat	ctc	gag	tat	ttg	agc	528	
Pro	Glu	Leu	Pro	Asn	Lys	Asp	Val	Lys	Leu	Asp	Leu	Glu	Tyr	Leu	Ser		
				165					170					175			
aga	aga	tcg	acc	ggc	ggc	gac	ttc	atc	atc	act	cag	atg	ttt	tac	gat	576	
Arg	Arg	Ser	Thr	Gly	Gly	Asp	Phe	Ile	Ile	Thr	Gln	Met	Phe	Tyr	Asp		
			180					185					190				
gtt	gat	aat	tta	ctc	aac	tgg	tgt	tcc	caa	gtt	aga	gct	gcg	ggc	atg	624	
Val	Asp	Asn	Leu	Leu	Asn	Trp	Cys	Ser	Gln	Val	Arg	Ala	Ala	Gly	Met		
		195				200						205					
gac	gtg	ccc	att	att	ccc	ggg	atc	atg	ccg	atc	act	acc	tac	gcg	gcc	672	
Asp	Val	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Thr	Tyr	Ala	Ala		
	210					215					220						
ttc	ttg	aga	agg	atc	caa	tgg	ggc	caa	atc	tcc	atc	cct	caa	cat	ttc	720	
Phe	Leu	Arg	Arg	Ile	Gln	Trp	Gly	Gln	Ile	Ser	Ile	Pro	Gln	His	Phe		
225					230					235					240		
tcg	tcc	cga	ttg	gat	cct	atc	aag	gac	gat	gac	gag	ttg	gtc	cgt	gat	768	
Ser	Ser	Arg	Leu	Asp	Pro	Ile	Lys	Asp	Asp	Asp	Glu	Leu	Val	Arg	Asp		
				245					250					255			
atc	gga	act	aac	ttg	atc	gtg	gaa	atg	tgt	caa	aaa	ttg	ctc	gac	agt	816	
Ile	Gly	Thr	Asn	Leu	Ile	Val	Glu	Met	Cys	Gln	Lys	Leu	Leu	Asp	Ser		
			260					265					270				
ggt	tac	gtt	tct	cac	ttg	cac	atc	tac	acc	atg	aac	ttg	gaa	aaa	gcg	864	
Gly	Tyr	Val	Ser	His	Leu	His	Ile	Tyr	Thr	Met	Asn	Leu	Glu	Lys	Ala		
		275					280						285				
cct	ctc	atg	att	ctg	gaa	aga	ttg	aac	att	cta	cct	acg	gaa	tca	gag	912	

Pro	Leu	Met	Ile	Leu	Glu	Arg	Leu	Asn	Ile	Leu	Pro	Thr	Glu	Ser	Glu	
290						295				300						
ttc	aat	gca	cat	cca	ttg	gcc	gtg	ttg	cca	tgg	aga	aaa	tct	ttg	aat	960
Phe	Asn	Ala	His	Pro	Leu	Ala	Val	Leu	Pro	Trp	Arg	Lys	Ser	Leu	Asn	
305					310				315						320	
cca	aag	cgt	aaa	aac	gag	gaa	gtc	aga	cct	atc	ttc	tgg	aag	aga	aga	1008
Pro	Lys	Arg	Lys	Asn	Glu	Glu	Val	Arg	Pro	Ile	Phe	Trp	Lys	Arg	Arg	
				325					330					335		
cct	tac	tcc	tat	gtc	gca	aga	acc	tct	caa	tgg	gcc	gtg	gac	gaa	ttc	1056
Pro	Tyr	Ser	Tyr	Val	Ala	Arg	Thr	Ser	Gln	Trp	Ala	Val	Asp	Glu	Phe	
			340					345					350			
ccc	aac	ggt	aga	ttc	ggt	gat	tcg	tct	tct	cct	gcg	ttc	ggt	gac	ttg	1104
Pro	Asn	Gly	Arg	Phe	Gly	Asp	Ser	Ser	Ser	Pro	Ala	Phe	Gly	Asp	Leu	
		355					360					365				
gat	ctg	tgt	ggt	tca	gac	ttg	atc	agg	caa	tca	gcg	aac	aaa	tgt	ctc	1152
Asp	Leu	Cys	Gly	Ser	Asp	Leu	Ile	Arg	Gln	Ser	Ala	Asn	Lys	Cys	Leu	
	370					375					380					
gaa	tta	tgg	tcc	acc	cct	act	tcc	atc	aac	gac	gtc	gcc	ttc	ttg	gtc	1200
Glu	Leu	Trp	Ser	Thr	Pro	Thr	Ser	Ile	Asn	Asp	Val	Ala	Phe	Leu	Val	
385					390					395					400	
atc	aac	tac	ttg	aat	gga	aac	ttg	aag	tgt	tta	cct	tgg	agt	gat	atc	1248
Ile	Asn	Tyr	Leu	Asn	Gly	Asn	Leu	Lys	Cys	Leu	Pro	Trp	Ser	Asp	Ile	
			405					410						415		
ccc	atc	aat	gat	gaa	ata	aat	cca	atc	aaa	gca	cac	ttg	att	gag	ctg	1296
Pro	Ile	Asn	Asp	Glu	Ile	Asn	Pro	Ile	Lys	Ala	His	Leu	Ile	Glu	Leu	
			420					425					430			
aac	cag	cat	tct	atc	atc	act	ata	aac	tct	caa	cct	caa	gtc	aac	ggc	1344
Asn	Gln	His	Ser	Ile	Ile	Thr	Ile	Asn	Ser	Gln	Pro	Gln	Val	Asn	Gly	
		435					440					445				
att	agg	tcc	aat	gac	aaa	att	cat	ggt	tgg	gga	ccc	aag	gat	ggt	tac	1392
Ile	Arg	Ser	Asn	Asp	Lys	Ile	His	Gly	Trp	Gly	Pro	Lys	Asp	Gly	Tyr	
	450					455				460						
gtt	tac	cag	aag	caa	tat	ttg	gaa	ttt	atg	ttg	ccc	aag	act	aag	ttg	1440
Val	Tyr	Gln	Lys	Gln	Tyr	Leu	Glu	Phe	Met	Leu	Pro	Lys	Thr	Lys	Leu	
465					470				475						480	
ccc	aag	ttg	att	gac	acc	ttg	aaa	aac	aat	gag	ttc	ttg	acc	tac	ttc	1488
Pro	Lys	Leu	Ile	Asp	Thr	Leu	Lys	Asn	Asn	Glu	Phe	Leu	Thr	Tyr	Phe	
				485					490					495		
gcc	atc	gac	tct	caa	ggt	gac	ctg	cta	agt	aat	cat	cca	gac	aac	tcc	1536
Ala	Ile	Asp	Ser	Gln	Gly	Asp	Leu	Leu	Ser	Asn	His	Pro	Asp	Asn	Ser	
			500					505					510			
aag	tcc	aac	gct	gtg	act	tgg	ggt	att	ttc	ccc	ggc	aga	gaa	att	ctt	1584
Lys	Ser	Asn	Ala	Val	Thr	Trp	Gly	Ile	Phe	Pro	Gly	Arg	Glu	Ile	Leu	
		515					520					525				
caa	cct	acc	att	gtc	gag	aaa	att	tcg	ttc	tta	gcg	tgg	aag	gag	gag	1632

Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu
 530 535 540

ttc tat cat atc ttg aat gaa tgg aaa cta aac atg aat aaa tac gat 1680
 Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp
 545 550 555 560

aaa ccg cat agt gcc caa ttc att cag tcc ttg att gac gat tac tgc 1728
 Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys
 565 570 575

ttg gtc aat att gtt gac aat gac tac att tct cca gat gat caa atc 1776
 Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile
 580 585 590

cat tcc atc cta cta agc cta taa 1800
 His Ser Ile Leu Leu Ser Leu
 595

<210> 24
 <211> 599
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 24
 Met Lys Ile Thr Glu Lys Leu Glu Gln His Arg Gln Thr Ser Gly Lys
 1 5 10 15

Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val
 20 25 30

Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro
 35 40 45

Gln Phe Ile Asp Ile Thr Trp Asn Ala Gly Gly Gly Arg Leu Ser His
 50 55 60

Leu Ser Thr Asp Leu Val Ala Thr Ala Gln Ser Val Leu Gly Leu Glu
 65 70 75 80

Thr Cys Met His Leu Thr Cys Thr Asn Met Pro Ile Ser Met Ile Asp
 85 90 95

Asp Ala Leu Glu Asn Ala Tyr His Ser Gly Cys Gln Asn Ile Leu Ala
 100 105 110

Leu Arg Gly Asp Pro Pro Arg Asp Ala Glu Asn Trp Thr Pro Val Glu
 115 120 125

Gly Gly Phe Gln Tyr Ala Lys Asp Leu Ile Lys Tyr Ile Lys Ser Lys
 130 135 140

Tyr Gly Asp His Phe Ala Ile Gly Val Ala Gly Tyr Pro Glu Cys His
 145 150 155 160

Pro Glu Leu Pro Asn Lys Asp Val Lys Leu Asp Leu Glu Tyr Leu Ser
 165 170 175

Arg Arg Ser Thr Gly Gly Asp Phe Ile Ile Thr Gln Met Phe Tyr Asp

180					185					190					
Val	Asp	Asn	Leu	Leu	Asn	Trp	Cys	Ser	Gln	Val	Arg	Ala	Ala	Gly	Met
		195					200						205		
Asp	Val	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Thr	Tyr	Ala	Ala
	210					215					220				
Phe	Leu	Arg	Arg	Ile	Gln	Trp	Gly	Gln	Ile	Ser	Ile	Pro	Gln	His	Phe
225					230					235					240
Ser	Ser	Arg	Leu	Asp	Pro	Ile	Lys	Asp	Asp	Asp	Glu	Leu	Val	Arg	Asp
				245					250					255	
Ile	Gly	Thr	Asn	Leu	Ile	Val	Glu	Met	Cys	Gln	Lys	Leu	Leu	Asp	Ser
			260					265					270		
Gly	Tyr	Val	Ser	His	Leu	His	Ile	Tyr	Thr	Met	Asn	Leu	Glu	Lys	Ala
		275					280					285			
Pro	Leu	Met	Ile	Leu	Glu	Arg	Leu	Asn	Ile	Leu	Pro	Thr	Glu	Ser	Glu
	290					295					300				
Phe	Asn	Ala	His	Pro	Leu	Ala	Val	Leu	Pro	Trp	Arg	Lys	Ser	Leu	Asn
305					310					315					320
Pro	Lys	Arg	Lys	Asn	Glu	Glu	Val	Arg	Pro	Ile	Phe	Trp	Lys	Arg	Arg
				325					330					335	
Pro	Tyr	Ser	Tyr	Val	Ala	Arg	Thr	Ser	Gln	Trp	Ala	Val	Asp	Glu	Phe
			340					345					350		
Pro	Asn	Gly	Arg	Phe	Gly	Asp	Ser	Ser	Ser	Pro	Ala	Phe	Gly	Asp	Leu
		355					360					365			
Asp	Leu	Cys	Gly	Ser	Asp	Leu	Ile	Arg	Gln	Ser	Ala	Asn	Lys	Cys	Leu
	370					375					380				
Glu	Leu	Trp	Ser	Thr	Pro	Thr	Ser	Ile	Asn	Asp	Val	Ala	Phe	Leu	Val
385					390					395					400
Ile	Asn	Tyr	Leu	Asn	Gly	Asn	Leu	Lys	Cys	Leu	Pro	Trp	Ser	Asp	Ile
				405					410					415	
Pro	Ile	Asn	Asp	Glu	Ile	Asn	Pro	Ile	Lys	Ala	His	Leu	Ile	Glu	Leu
			420					425					430		
Asn	Gln	His	Ser	Ile	Ile	Thr	Ile	Asn	Ser	Gln	Pro	Gln	Val	Asn	Gly
		435					440					445			
Ile	Arg	Ser	Asn	Asp	Lys	Ile	His	Gly	Trp	Gly	Pro	Lys	Asp	Gly	Tyr
	450					455					460				
Val	Tyr	Gln	Lys	Gln	Tyr	Leu	Glu	Phe	Met	Leu	Pro	Lys	Thr	Lys	Leu
465					470					475					480
Pro	Lys	Leu	Ile	Asp	Thr	Leu	Lys	Asn	Asn	Glu	Phe	Leu	Thr	Tyr	Phe
				485					490					495	
Ala	Ile	Asp	Ser	Gln	Gly	Asp	Leu	Leu	Ser	Asn	His	Pro	Asp	Asn	Ser

500	505	510
Lys Ser Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Leu 515	520	525
Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu 530	535	540
Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp 545	550	555
Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys 565	570	575
Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile 580	585	590
His Ser Ile Leu Leu Ser Leu 595		

<210> 25
 <211> 897
 <212> DNA
 <213> Erwinia carotovora

<220>
 <221> CDS
 <222> (1)..(894)
 <223> RE000089

<400> 25	
atg agc ttt ttt cac gca aac cag cgg gaa gcg ctg aat caa agt ctg	48
Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu	
1 5 10 15	
gcg gaa ttg cag gga cga att aat gtg tca ttt gaa ttt ttc ccg cca	96
Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgt acc agc gat atg gaa gaa acc ctg tgg agc tct atc gat cga ctg	144
Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu	
35 40 45	
agc agc ctg aag ccc aag ttt gtt tcc gtg act tac ggg gcg aat tct	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
ggc gag cgt gac cgt act cac agc att atc aaa acg att aaa gag cgt	240
Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Thr Ile Lys Glu Arg	
65 70 75 80	
acc ggt ctg gaa gcg gca cct cac ctg acc tgc atc gat gct tca cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg	
85 90 95	
gaa cag ctg cgt gaa atc gct cag gat tac tgg gag agt ggt atc cgc	336
Glu Gln Leu Arg Glu Ile Ala Gln Asp Tyr Trp Glu Ser Gly Ile Arg	
100 105 110	

cat att gtc gcg ctg cgc ggc gac ttg cct caa gaa ggc ggc aaa ccg 384
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Gln Glu Gly Gly Lys Pro
 115 120 125

gac atg tac gcg gcg gat ctg gtt tcc ctg ctg aaa gag gtc ggt gat 432
 Asp Met Tyr Ala Ala Asp Leu Val Ser Leu Leu Lys Glu Val Gly Asp
 130 135 140

ttc gat att tcc gtt gcc gcc tat cct gaa gta cac cct gaa gcg aaa 480
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

agc gcg cag gct gac ctg att aac ctg aaa cac aag att gat gcc ggc 528
 Ser Ala Gln Ala Asp Leu Ile Asn Leu Lys His Lys Ile Asp Ala Gly
 165 170 175

gcg aat cgc gct atc aca cag ttc ttt ttc gac gta gaa agc tat ttg 576
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190

cgg ttc cgt gac cgc tgc gtg gca acg ggc atc gat gta gaa att gtg 624
 Arg Phe Arg Asp Arg Cys Val Ala Thr Gly Ile Asp Val Glu Ile Val
 195 200 205

ccg ggc att ctg cca gta tgc aac ttc aaa cag ttg cag aaa ttt gcc 672
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Leu Gln Lys Phe Ala
 210 215 220

acg atg acc aac gtc cgt gtg ccg aac tgg atg acg acc atg ttt gac 720
 Thr Met Thr Asn Val Arg Val Pro Asn Trp Met Thr Thr Met Phe Asp
 225 230 235 240

ggc ctg gat aac gat cca gaa acc cgc aaa atg gtg ggg gcg tct atc 768
 Gly Leu Asp Asn Asp Pro Glu Thr Arg Lys Met Val Gly Ala Ser Ile
 245 250 255

gcc atg gat atg gtg aaa att ctc agc cgc gaa ggc gta aaa gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cat ttc tat acg ctg aac cgc gcg gag ctg agc tat gcg att tgc cat 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Leu Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gtc cgc cct gat gta gca cgc tga 897
 Thr Leu Gly Val Arg Pro Asp Val Ala Arg
 290 295

<210> 26

<211> 298

<212> PRT

<213> *Erwinia carotovora*

<400> 26

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg	Thr	Ser	Asp	Met	Glu	Glu	Thr	Leu	Trp	Ser	Ser	Ile	Asp	Arg	Leu
		35					40					45			
Ser	Ser	Leu	Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser
	50					55					60				
Gly	Glu	Arg	Asp	Arg	Thr	His	Ser	Ile	Ile	Lys	Thr	Ile	Lys	Glu	Arg
65					70					75					80
Thr	Gly	Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Cys	Ile	Asp	Ala	Ser	Arg
				85					90					95	
Glu	Gln	Leu	Arg	Glu	Ile	Ala	Gln	Asp	Tyr	Trp	Glu	Ser	Gly	Ile	Arg
			100					105					110		
His	Ile	Val	Ala	Leu	Arg	Gly	Asp	Leu	Pro	Gln	Glu	Gly	Gly	Lys	Pro
		115					120					125			
Asp	Met	Tyr	Ala	Ala	Asp	Leu	Val	Ser	Leu	Leu	Lys	Glu	Val	Gly	Asp
		130				135					140				
Phe	Asp	Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys
145					150					155					160
Ser	Ala	Gln	Ala	Asp	Leu	Ile	Asn	Leu	Lys	His	Lys	Ile	Asp	Ala	Gly
				165					170					175	
Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu
			180					185					190		
Arg	Phe	Arg	Asp	Arg	Cys	Val	Ala	Thr	Gly	Ile	Asp	Val	Glu	Ile	Val
		195					200					205			
Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn	Phe	Lys	Gln	Leu	Gln	Lys	Phe	Ala
	210					215					220				
Thr	Met	Thr	Asn	Val	Arg	Val	Pro	Asn	Trp	Met	Thr	Thr	Met	Phe	Asp
225				230						235					240
Gly	Leu	Asp	Asn	Asp	Pro	Glu	Thr	Arg	Lys	Met	Val	Gly	Ala	Ser	Ile
				245					250					255	
Ala	Met	Asp	Met	Val	Lys	Ile	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe
			260					265					270		
His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala	Glu	Leu	Ser	Tyr	Ala	Ile	Cys	His
		275					280					285			
Thr	Leu	Gly	Val	Arg	Pro	Asp	Val	Ala	Arg						
	290					295									

```
<210> 27
<211> 888
<212> DNA
<213> Klebsiella pneumoniae
```

<220>
<221> CDS

<222> (1)..(885)

<223> RKP07488

<400> 27

atg agc ttt ttt cac gcc aat cag cgg gaa gcc ctg aat cag agc ctg	48
Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu	
1 5 10 15	
gcg gaa gtc cag ggc cag att aat gtg tct ttt gaa ttc ttt ccg ccg	96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgc acc agt gaa atg gag caa acc ctg tgg aaa tcc atc gat cgc ctg	144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu	
35 40 45	
agc agt ctg aaa ccg aag ttt gtt tgc gta acc tat ggc gcg aac tct	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
ggc gag cgc gat cgc acc cac agc atc atc aaa ggc att aaa gag cga	240
Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
acc ggt ctg gaa gca gcg ccg cac ctg acc tgt atc gat gcc agc cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg	
85 90 95	
gat gag ttg cgc act atc gct cag gat tac tgg aac aac ggt atc cgc	336
Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cat atc gtc gcc ctg cgc ggc gac ctg ccg ccg ggc agc ggt aaa ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gat atg tac gcc gcc gat ctg gtg acg ttg ctg aaa gag gta ggc gat	432
Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp	
130 135 140	
ttt gat atc tct gtc gcc gcg tat ccg gaa gtg cat ccg gag gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gcg cag gcg gat tta ctg aac ctg aag cgc aaa gta gaa gca ggg	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly	
165 170 175	
gcc aac cgc gcg atc acc cag ttc ttc ttc gat gtg gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgc gat cgc tgc gtc tgc gca ggc atc gac gtg gaa atc att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccc ggt atc ctg ccg gtc tcc aac ttt aaa cag gcg aaa aag ttt gcg	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	

gat atg acc aac gtc cgt atc ccg gtg tgg atg tca aaa atg ttc gaa 720
 Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu
 225 230 235 240

ggg ctg gat aac gac gcc gaa acc cgt caa ctg gtg ggg gcg aat atc 768
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile
 245 250 255

gcc atg gac atg gtg aag atc tta agc cgg gaa ggg gtc aag gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cac ttc tac acc ctg aac cgc gcc gag atg agc tac gcc atc tgc cat 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gta cgc ccg gcc tga 888
 Thr Leu Gly Val Arg Pro Ala
 290 295

<210> 28

<211> 295

<212> PRT

<213> *Klebsiella pneumoniae*

<400> 28

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg
 85 90 95

Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp
 130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly
 165 170 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
210 215 220

Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu
225 230 235 240

Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile
245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
275 280 285

Thr Leu Gly Val Arg Pro Ala
290 295

<210> 29

<211> 891

<212> DNA

<213> Salmonella typhi

<220>

<221> CDS

<222> (1)..(888)

<223> RTY02485

<400> 29

atg agc ttt ttt cac gcc aac cag cgg gaa gcc ctg aat cag agc ctg	48
Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu	
1 5 10 15	
gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg	96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg	144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu	
35 40 45	
agc agc ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
ggg gaa cgt gac cgc act cat agt gtt att aaa ggc att aaa gag cgt	240
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg	
85 90 95	

gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc 336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
100 105 110

cac att gtt gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg 384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
115 120 125

gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gtc gat 432
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp
130 135 140

ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa 480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
145 150 155 160

agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc 528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
165 170 175

gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tat ctg 576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
180 185 190

cgt ttt cgc gac cgc tgt gtt tcc gcc ggt atc gac gta gaa att att 624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
195 200 205

ccc ggc att tta ccg gtg tct aac ttt aaa cag gcg aaa aaa ttt gcc 672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
210 215 220

gat atg acc aat gtc cgc att ccg tcc tgg atg tcg ctg atg ttt gag 720
Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
225 230 235 240

ggg ctg gat gat gac gca gaa acc cgc aag ctg gtg ggc gct aac att 768
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
245 250 255

gcg atg gac atg gtg aaa att tta agc cgc gaa gga gtg aag gat ttc 816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
260 265 270

cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac 864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
275 280 285

acg ctg ggc gta aga ccg ggt tta taa 891
Thr Leu Gly Val Arg Pro Gly Leu
290 295

<210> 30

<211> 296

<212> PRT

<213> Salmonella typhi

<400> 30

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu

1	5	10	15
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	20	25	30
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu	35	40	45
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	50	55	60
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg	65	70	75
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg	85	90	95
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	100	105	110
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	115	120	125
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp	130	135	140
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	145	150	155
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	165	170	175
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	180	185	190
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	195	200	205
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	210	215	220
Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu	225	230	235
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	245	250	255
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	260	265	270
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	275	280	285
Thr Leu Gly Val Arg Pro Gly Leu	290	295	

<210> 31
 <211> 891
 <212> DNA

<213> *Salmonella typhimurium*

<220>

<221> CDS

<222> (1)..(888)

<223> RSY00593

<400> 31

atg agc ttt ttt cac gcc aac cag cgg gaa gcc ctg aat cag agc ctg	48
Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu	
1 5 10 15	
gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg	96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg	144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu	
35 40 45	
agc agt ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
ggg gaa cgc gac cgc acc cat agc gtt att aaa ggc atc aaa gag cgt	240
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg	
85 90 95	
gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc	336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cac att gtc gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gcc gat	432
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp	
130 135 140	
ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgc gac cgc tgt gtt tct gcc ggt atc gac gta gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	

ccc ggc att tta ccg gtg tct aac ttt aaa cag gca aaa aaa ttt gcc 672
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220

gat atg acc aat gtc cgc att ccg tcc tgg atg tca ctg atg ttt gag 720
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240

ggg ctg gat aat gac gca gaa acc cgc aag ctg gtg ggc gct aac att 768
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255

gcg atg gac atg gtg aaa att tta agc cgt gaa gga gtg aag gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gta aga ccg ggt tta taa 891
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 32

<211> 296

<212> PRT

<213> Salmonella typhimurium

<400> 32

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
 85 90 95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp
 130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 33
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(888)
 <223> REC03839

<400> 33
 atg agc ttt ttt cac gcc agc cag cgg gat gcc ctg aat cag agc ctg 48
 Met Ser Phe Phe His Ala Ser Gln Arg Asp Ala Leu Asn Gln Ser Leu
 1 5 10 15
 gca gaa gtc cag ggg cag att aac gtt tgc ttc gag ttt ttc ccg ccg 96
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 cgt acc agt gaa atg gag cag acc ctg tgg aac tcc atc gat cgc ctt 144
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45
 agc agc ctg aaa ccg aag ttt gta tgc gtg acc tat ggc gcg aac tcc 192
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60
 ggc gag cgc gac cgt acg cac agc att att aaa ggc att aaa gat cgc 240
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg
 65 70 75 80

act ggt ctg gaa gcg gca ccg cat ctt act tgc att gat gcg acg ccc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro	
85 90 95	
gac gag ctg cgc acc att gca cgc gac tac tgg aat aac ggt att cgt	336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cat atc gtg gcg ctg cgt ggc gat ctg ccg ccg gga agt ggt aag cca	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gaa atg tat gct tct gac ctg gtg acg ctg tta aaa gaa gtg gca gat	432
Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp	
130 135 140	
ttc gat atc tcc gtg gcg gcg tat ccg gaa gtt cac ccg gaa gca aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gct cag gcg gat ttg ctt aat ctg aaa cgc aaa gtg gat gcc gga	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
gcc aac cgc gcg att act cag ttc ttc ttc gat gtc gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgt gac cgc tgt gta tgc gcg ggc att gat gtg gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccg gga att ttg ccg gta tct aac ttt aaa cag gcg aag aaa ttt gcc	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	
gat atg acc aac gtg cgt att ccg gcg tgg atg gcg caa atg ttc gac	720
Asp Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp	
225 230 235 240	
ggt ctg gat gat gat gcc gaa acc cgc aaa ctg gtt ggc gcg aat att	768
Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	
245 250 255	
gcc atg gat atg gtg aag att tta agc cgt gaa gga gtg aaa gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	
cac ttc tat acg ctt aac cgt gct gaa atg agt tac gcg att tgc cat	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	
275 280 285	
acg ctg ggg gtt cga cct ggt tta taa	891
Thr Leu Gly Val Arg Pro Gly Leu	
290 295	

<210> 34

<211> 296

<212> PRT

<213> Escherichia coli

<400> 34

```

Met Ser Phe Phe His Ala Ser Gln Arg Asp Ala Leu Asn Gln Ser Leu
  1              5              10              15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
      20              25              30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
      35              40              45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
      50              55              60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg
      65              70              75              80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro
      85              90              95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
      100             105             110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
      115             120             125

Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp
      130             135             140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
      145             150             155             160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
      165             170             175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
      180             185             190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
      195             200             205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
      210             215             220

Asp Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp
      225             230             235             240

Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
      245             250             255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
      260             265             270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
      275             280             285

Thr Leu Gly Val Arg Pro Gly Leu
      290             295

```


<210> 35
 <211> 915
 <212> DNA
 <213> *Vibrio cholerae*

<220>
 <221> CDS
 <222> (1)..(912)
 <223> RVC06433

<400> 35
 gtg aca ctc ggt cac agg gag tac aag atg gga tac aca cac gct agc 48
 Val Thr Leu Gly His Arg Glu Tyr Lys Met Gly Tyr Thr His Ala Ser
 1 5 10 15

cat atc gat gca ttg aac caa aac att gcg gag ctt tcc gac atc aat 96
 His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn
 20 25 30

gtt tcg ttt gag ttt ttt cca ccc agc tca cca caa atg gaa gaa acg 144
 Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr
 35 40 45

ctt tgg gga tcg gta cac cgt ctg aaa aca ctc caa ccg aaa ttt gtt 192
 Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val
 50 55 60

tcg gtc act tat ggt gca aac tct ggt gag cgt gac cgt act cac tcg 240
 Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser
 65 70 75 80

atc att aaa gcg atc aaa gat caa acc ggt tta att gcc gcg cca cac 288
 Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His
 85 90 95

ctg act tgt atc gat gcc act cgt gat gaa ctg atc cag atc gcc gat 336
 Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp
 100 105 110

gac tac tgg cat aac ggc atc cag aat att gtg gcg ctg cgt ggg gat 384
 Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp
 115 120 125

atc ccg gct ggc ggt ggt aag cca gag atg tac gcc tcc gat cta gtg 432
 Ile Pro Ala Gly Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val
 130 135 140

acg ctg ctc aaa tca cgc cac gat ttt gat att tcc gtg gcc gcc ttc 480
 Thr Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe
 145 150 155 160

cct gaa gtg cac cct gaa gcc aaa agc gcg caa gcg gac ctg ctc aat 528
 Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn
 165 170 175

tta aaa cgt aaa gtc gat gca ggt gcg aat cgt gcc atc acg cag ttt 576
 Leu Lys Arg Lys Val Asp Ala Gly Ala Asn Arg Ala Ile Thr Gln Phe
 180 185 190

```

ttc ttt gat gta gaa agc tac ctg cgt ttt cgc gat cgc tgt gtg gcc 624
Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala
      195                200                205

gct ggg att gac gta gaa atc gtg cct ggc att ctg ccg gtt tct aac 672
Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn
      210                215                220

ttt aaa caa gcg tcg cgc ttc gct gcg caa aac aac gtc aaa gtt ccg 720
Phe Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro
      225                230                235                240

aat tgg atg gtg aag cag ttt gaa gga tta gaa gac gat cca gtg act 768
Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr
      245                250                255

cgc cag ttg gta ggt gca agc caa gcc att gat atg gtg cgc gtg ctg 816
Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu
      260                265                270

tgc cgt gaa ggg gtg aag gat ttc cac ttc tac acc cta aat cgt gcc 864
Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala
      275                280                285

gaa atg act tac gcg tta tgc cac acc tta ggc gtt cgc cca caa gct 912
Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala
      290                295                300

taa 915

```

```

<210> 36
<211> 304
<212> PRT
<213> Vibrio cholerae

```

```

<400> 36
Val Thr Leu Gly His Arg Glu Tyr Lys Met Gly Tyr Thr His Ala Ser
  1                5                10                15

His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn
      20                25                30

Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr
      35                40                45

Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val
      50                55                60

Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser
      65                70                75                80

Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His
      85                90                95

Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp
      100                105                110

Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp

```

115	120	125
Ile Pro Ala Gly Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val 130 135 140		
Thr Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe 145 150 155 160		
Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn 165 170 175		
Leu Lys Arg Lys Val Asp Ala Gly Ala Asn Arg Ala Ile Thr Gln Phe 180 185 190		
Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala 195 200 205		
Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn 210 215 220		
Phe Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro 225 230 235 240		
Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr 245 250 255		
Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu 260 265 270		
Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala 275 280 285		
Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala 290 295 300		

<210> 37
 <211> 879
 <212> DNA
 <213> Haemophilus influenzae

<220>
 <221> CDS
 <222> (1)..(876)
 <223> RHI06620

<400> 37	
atg agc tac gcg aaa gaa att gat aca tta aat caa cat att gca gat Met Ser Tyr Ala Lys Glu Ile Asp Thr Leu Asn Gln His Ile Ala Asp 1 5 10 15	48
ttt aat aaa aaa att aat gtc tcc ttt gaa ttt ttt cca cct aaa aac Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn 20 25 30	96
gaa aaa atg gaa acc ctt cta tgg gat tca att cat cgt tta aaa gta Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val	144

35	40	45	
tta aag cct aaa ttt gtg tca gtc act tac ggt gca aat tcg gga gaa Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu 50 55 60			192
cgt gac cgc act cac ggc att gtg aaa gcc att aaa caa gaa act ggc Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly 65 70 75 80			240
tta gaa gcc gca cca cat tta act gga att gat gcc aca cct gaa gaa Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu 85 90 95			288
tta aaa caa att gcg aga gat tat tgg gat agt ggt att cgc cgt att Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile 100 105 110			336
gtt gcg tta cgc ggt gac gaa cct aaa ggt tac gcg aaa aaa cca ttt Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe 115 120 125			384
tat gcg tca gat ctt gtg gaa tta ctc cgt tct gtc gct gat ttt gat Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp 130 135 140			432
att tct gta gcc gct tat ccc gaa gtt cat cca gaa gca aaa tcc gca Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala 145 150 155 160			480
caa gca gac tta att aat tta aaa cgt aaa att gat gca ggt gca aac Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn 165 170 175			528
cac gtc att aca caa ttt ttc ttt gat att gaa aac tac cta cgt ttt His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe 180 185 190			576
cgt gat cgt tgt gca tca att ggt att gat act gaa atc gta ccc ggt Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly 195 200 205			624
att tta cct gtt act aat ttt aaa caa ctc caa aaa atg gca tca ttc Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe 210 215 220			672
act aat gtg aaa att cca gcg tgg tta gtt aaa gcc tat gat ggt ttg Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu 225 230 235 240			720
gat aat gat cca act aca cgt aat ctt gtg gca gca agt gtt gca atg Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met 245 250 255			768
gat atg gta aaa att tta tct cgc gaa ggc gtg aat gac ttc cac ttt Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe 260 265 270			816
tat aca tta aat cgt agt gaa tta act tat gct atc tgt cat atg tta Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu			864

275 280 285
 ggt gta aga cct taa
 Gly Val Arg Pro
 290

879

<210> 38
 <211> 292
 <212> PRT
 <213> Haemophilus influenzae

<400> 38
 Met Ser Tyr Ala Lys Glu Ile Asp Thr Leu Asn Gln His Ile Ala Asp
 1 5 10 15

Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn
 20 25 30

Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val
 35 40 45

Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60

Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu
 85 90 95

Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe
 115 120 125

Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe
 180 185 190

Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly
 195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe
 210 215 220

Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu
 225 230 235 240

Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met

	245		250		255	
Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe						
	260		265		270	
Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu						
	275		280		285	
Gly Val Arg Pro						
	290					

<210> 39
 <211> 945
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
 <221> CDS
 <222> (1) .. (942)
 <223> RCO02274

<400> 39	
atg acc ctt ccg ccc acc cgc cgc gtg atc ggt ccc gtc gcc cga gcc	48
Met Thr Leu Pro Pro Thr Arg Arg Val Ile Gly Pro Val Ala Arg Ala	
1 5 10 15	
ggc gag cgg acc ggc cgt ccg cgc gtg tcg ttc gag ttc ttc ccg ccc	96
Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
aag act ccg cag atg gaa gag agc ctg tgg cag gcg atc aca cgc ctg	144
Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu	
35 40 45	
gcg ccg ctg gat ccg gcc ttc gtc tcg gtg acc tat ggc gcg ggc ggc	192
Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly	
50 55 60	
tcc acc cgc gag cgc acc cac cgc acc gtc aag cgg atc ctg gac gag	240
Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu	
65 70 75 80	
acc agc ctc aag ccc gcc gcg cac ctg acc tgc gtc ggc gcc agt cgc	288
Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg	
85 90 95	
gaa gag gtc gat gag gtc att cgc gag tac tgg gag acc ggg gtc cgt	336
Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg	
100 105 110	
cac atc gtt tcg ctg cgg ggc gat ccg ccg ccc ggc gag ggc ggc atc	384
His Ile Val Ser Leu Arg Gly Asp Pro Pro Pro Gly Glu Gly Gly Ile	
115 120 125	
ggc ggg gtc tat gtg ccg cgc gcc gac ggc tac gcc aac gcc aca gag	432
Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu	
130 135 140	
ttg acc aag gcc gtg cgc gcg atc gcg ccg ttc gag gtg ctg gtc ggg	480

Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly
 145 150 155 160
 gtc tat ccc gag aag cat ccc gag agc ccc tcg ttg gag cac gac atc 528
 Val Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile
 165 170 175
 gac gtc ttg aag cag aag gtc gac gcc ggc gcg acg ctg ggg atc agc 576
 Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser
 180 185 190
 cag ttc ttc ttc gac ctc gac gcc ttc ctg cgc ttc gtc gac aag gtg 624
 Gln Phe Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val
 195 200 205
 cgc gcg gcg ggc atc acc att ccg atc gtg ccg ggg atc atg ccg gtg 672
 Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val
 210 215 220
 acc aat ttc gcg ggc ttg aag aag atg gcc gcc gcc tgc cag acg gcc 720
 Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala
 225 230 235 240
 atc ccg tcc tgg ctg ggg aac ctg ttc gac ggg ctg gag aac gac gcg 768
 Ile Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala
 245 250 255
 gag acc cgc cgc ctg atc gcc tgt tcg gtg gcc gcc gag atg tgc gcc 816
 Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala
 260 265 270
 aag ctg cag gaa cag ggt ttc gag gac ttc cac ttc tac acc ctg aac 864
 Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn
 275 280 285
 cgg gcc gat ctc gtt tac gcc atc tgc cgt gtg ctg ggc gtg cgc gag 912
 Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu
 290 295 300
 atc tcg ccc gcc gct tcg gag gtc gcc gca tga 945
 Ile Ser Pro Ala Ala Ser Glu Val Ala Ala
 305 310

<210> 40

<211> 314

<212> PRT

<213> *Caulobacter crescentus*

<400> 40

Met Thr Leu Pro Pro Thr Arg Arg Val Ile Gly Pro Val Ala Arg Ala
 1 5 10 15
 Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu
 35 40 45
 Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly

	50						55							60							
Ser 65	Thr	Arg	Glu	Arg	Thr 70	His	Arg	Thr	Val	Lys 75	Arg	Ile	Leu	Asp	Glu 80						
Thr	Ser	Leu	Lys	Pro 85	Ala	Ala	His	Leu	Thr	Cys	Val	Gly	Ala	Ser	Arg						
Glu	Glu	Val	Asp 100	Glu	Val	Ile	Arg	Glu	Tyr	Trp	Glu	Thr	Gly	Val	Arg						
His	Ile	Val 115	Ser	Leu	Arg	Gly	Asp 120	Pro	Pro	Pro	Gly	Glu 125	Gly	Gly	Ile						
Gly	Gly 130	Val	Tyr	Val	Pro	Arg 135	Ala	Asp	Gly	Tyr	Ala 140	Asn	Ala	Thr	Glu						
Leu 145	Thr	Lys	Ala	Val 150	Arg	Ala	Ile	Ala	Pro	Phe 155	Glu	Val	Leu	Val	Gly 160						
Val	Tyr	Pro	Glu	Lys 165	His	Pro	Glu	Ser	Pro	Ser	Leu	Glu	His	Asp 175	Ile						
Asp	Val	Leu	Lys 180	Gln	Lys	Val	Asp	Ala 185	Gly	Ala	Thr	Leu	Gly	Ile	Ser						
Gln	Phe	Phe 195	Phe	Asp	Leu	Asp	Ala 200	Phe	Leu	Arg	Phe	Val 205	Asp	Lys	Val						
Arg 210	Ala	Ala	Gly	Ile	Thr	Ile 215	Pro	Ile	Val	Pro	Gly 220	Ile	Met	Pro	Val						
Thr 225	Asn	Phe	Ala	Gly 230	Leu	Lys	Lys	Met	Ala 235	Ala	Ala	Cys	Gln	Thr	Ala 240						
Ile	Pro	Ser	Trp	Leu 245	Gly	Asn	Leu	Phe	Asp 250	Gly	Leu	Glu	Asn	Asp 255	Ala						
Glu	Thr	Arg	Arg 260	Leu	Ile	Ala	Cys	Ser	Val 265	Ala	Ala	Glu	Met	Cys	Ala						
Lys	Leu	Gln 275	Glu	Gln	Gly	Phe	Glu 280	Asp	Phe	His	Phe	Tyr 285	Thr	Leu	Asn						
Arg 290	Ala	Asp	Leu	Val	Tyr	Ala 295	Ile	Cys	Arg	Val	Leu 300	Gly	Val	Arg	Glu						
Ile 305	Ser	Pro	Ala	Ala	Ser	Glu	Val	Ala	Ala												

```
<210> 41
<211> 885
<212> DNA
<213> Actinobacillus actinomycetemcomitans
```

```
<220>  
<221> CDS  
<222> (1) .. (882)
```


<223> RAB00260

<400> 41

atg agt tac gca aaa gaa att gat aat cta aat caa cat tta gct gat	48
Met Ser Tyr Ala Lys Glu Ile Asp Asn Leu Asn Gln His Leu Ala Asp	
1 5 10 15	
tta aac ggc aaa att aat gtc tct ttt gaa ttt ttc ccg ccg aaa agt	96
Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser	
20 25 30	
gaa aaa atg gaa aat ctt ctg tgg gaa tcc atc cat cgc tta aaa gtg	144
Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val	
35 40 45	
cta aaa ccg aaa ttt gta tcc gtg act tac ggc gcc aat tcc ggc gag	192
Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
cgt gaa cgc act cac ggg gtg gtg aaa cgc att aag cag gaa acc ggt	240
Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly	
65 70 75 80	
ctg gaa gct gcg ccg cat tta acc ggt att gac gct acc tcg gac gaa	288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu	
85 90 95	
ttg cgt cgc att gcc aaa ggt tat tgg gat agc ggc att cgt cgc att	336
Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
gtg gca ctg cgc ggt gac gag ccg aaa ggc tac gag aaa aaa cca ttt	384
Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe	
115 120 125	
tat gcc gcc gat tta gta gca tta tta cgt gac gta tca gat ttt gat	432
Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp	
130 135 140	
att tcc gtg gcg gca tac cct gag gtt cat ccg gaa gcc aaa tcg gcg	480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
caa gcg gat tta att aat tta aaa cgt aaa att gat gcc ggt gcc aat	528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	
cat gtg atc aca caa ttc ttt ttc gat att gac agc tat ctg cgg ttc	576
His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe	
180 185 190	
cgc gat cgc tgc gcg tct atc ggt att gat gca gaa atc gtg ccg ggg	624
Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Ala Glu Ile Val Pro Gly	
195 200 205	
att ctg ccg gtg acc aac ttc aaa caa tta caa aaa atg gca gca atc	672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ala Ile	
210 215 220	
act aat gtg aaa att cca gct tgg atg agc aaa atg tat gaa ggc ttg	720

Thr Asn Val Lys Ile Pro Ala Trp Met Ser Lys Met Tyr Glu Gly Leu
 225 230 235 240

gat gat gac caa acc acc cgc aat ctg gtg gcg gcg agc atc gcc atg 768
 Asp Asp Asp Gln Thr Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Met
 245 250 255

gac atg gtg cgt gta ctg tcc cgc gaa ggg gta aaa gac ttt cat ttc 816
 Asp Met Val Arg Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270

tac acc ctg aat cgc agt gaa ctc acc tat gct att tgc cac acg tta 864
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Thr Leu
 275 280 285

ggc att cgt ccg agt ttg taa 885
 Gly Ile Arg Pro Ser Leu
 290

<210> 42
 <211> 294
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 42
 Met Ser Tyr Ala Lys Glu Ile Asp Asn Leu Asn Gln His Leu Ala Asp
 1 5 10 15

Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser
 20 25 30

Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val
 35 40 45

Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60

Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu
 85 90 95

Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe
 115 120 125

Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe

180					185					190						
Arg	Asp	Arg	Cys	Ala	Ser	Ile	Gly	Ile	Asp	Ala	Glu	Ile	Val	Pro	Gly	
195					200					205						
Ile	Leu	Pro	Val	Thr	Asn	Phe	Lys	Gln	Leu	Gln	Lys	Met	Ala	Ala	Ile	
210					215					220						
Thr	Asn	Val	Lys	Ile	Pro	Ala	Trp	Met	Ser	Lys	Met	Tyr	Glu	Gly	Leu	
225					230					235					240	
Asp	Asp	Asp	Gln	Thr	Thr	Arg	Asn	Leu	Val	Ala	Ala	Ser	Ile	Ala	Met	
245					250					255						
Asp	Met	Val	Arg	Val	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe	His	Phe	
260					265					270						
Tyr	Thr	Leu	Asn	Arg	Ser	Glu	Leu	Thr	Tyr	Ala	Ile	Cys	His	Thr	Leu	
275					280					285						
Gly	Ile	Arg	Pro	Ser	Leu											
290																

<210> 43
 <211> 867
 <212> DNA
 <213> Rhodobacter

<220>
 <221> CDS
 <222> (1)..(864)
 <223> RRC03981

<400> 43		
atg acc acg ccg cat gtc agc ttt gaa ttc ttc ccg ccg cag acg ctc	48	
Met Thr Thr Pro His Val Ser Phe Glu Phe Phe Pro Pro Gln Thr Leu		
1 5 10 15		
gac gcc tcg ttc cgg ctg tgg gag acg gcg cag gtt ctg gcg ccg ctc	96	
Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu		
20 25 30		
aag ccc ggc ttc gtc tcg gtc acc tat ggc gcg ggc ggc acc acc cgc	144	
Lys Pro Gly Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Thr Thr Arg		
35 40 45		
aag ctg acg cat gag gcc gtg gcg gcg atc cac aag aat tac ggc ctg	192	
Lys Leu Thr His Glu Ala Val Ala Ala Ile His Lys Asn Tyr Gly Leu		
50 55 60		
aac gtc gcc gcg cat ctg acc tgc gtc gat gcg acc cgg gcc gaa acg	240	
Asn Val Ala Ala His Leu Thr Cys Val Asp Ala Thr Arg Ala Glu Thr		
65 70 75 80		
caa gag atc atc gac gcc tat gcc gag gct ggc gtc acc gag att gtc	288	
Gln Glu Ile Ile Asp Ala Tyr Ala Glu Ala Gly Val Thr Glu Ile Val		
85 90 95		
gcg ctg cgc ggt gat ccg ccg aaa ggc gcc gcc cgc ttc acg ccg cat	336	

Ala	Leu	Arg	Gly	Asp	Pro	Pro	Lys	Gly	Ala	Ala	Arg	Phe	Thr	Pro	His		
			100					105					110				
ccg	gac	ggg	ttt	gcc	tcc	tcg	gtg	gac	ctc	atc	gaa	tgg	ctg	gcg	cgg	384	
Pro	Asp	Gly	Phe	Ala	Ser	Ser	Val	Asp	Leu	Ile	Glu	Trp	Leu	Ala	Arg		
		115					120				125						
gac	ggc	cgc	ttc	acg	ctg	cgc	tgc	ggc	gcc	tat	ccg	gaa	ccg	cat	ccg	432	
Asp	Gly	Arg	Phe	Thr	Leu	Arg	Cys	Gly	Ala	Tyr	Pro	Glu	Pro	His	Pro		
	130					135				140							
gaa	gcc	gcc	gac	acg	ctg	gcc	gac	gtg	cgc	tgg	ctg	aaa	cgc	aaa	tgc	480	
Glu	Ala	Ala	Asp	Thr	Leu	Ala	Asp	Val	Arg	Trp	Leu	Lys	Arg	Lys	Cys		
145					150				155						160		
gag	gcg	ggg	gcg	acc	tcg	gcg	atc	acg	caa	ttc	ttc	ttt	gaa	gcc	gag	528	
Glu	Ala	Gly	Ala	Thr	Ser	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Glu	Ala	Glu		
			165					170					175				
acc	ttc	ttc	cgc	ttc	cgc	gac	gcc	tgc	gtg	aag	gaa	ggg	atc	acc	gcc	576	
Thr	Phe	Phe	Arg	Phe	Arg	Asp	Ala	Cys	Val	Lys	Glu	Gly	Ile	Thr	Ala		
			180					185					190				
aag	atc	atc	ccg	ggc	atc	ctg	ccg	atc	cag	tcc	tgg	aaa	ggc	gcc	aag	624	
Lys	Ile	Ile	Pro	Gly	Ile	Leu	Pro	Ile	Gln	Ser	Trp	Lys	Gly	Ala	Lys		
	195					200					205						
agc	ttt	gcg	cag	cgc	tgc	ggc	acc	tcg	atc	ccg	acc	tgg	gtc	gaa	gag	672	
Ser	Phe	Ala	Gln	Arg	Cys	Gly	Thr	Ser	Ile	Pro	Thr	Trp	Val	Glu	Glu		
	210				215					220							
gcc	ttt	gac	cat	gcg	atc	cgc	gac	gac	cgc	gaa	cag	ctg	ctg	gcc	acg	720	
Ala	Phe	Asp	His	Ala	Ile	Arg	Asp	Asp	Arg	Glu	Gln	Leu	Leu	Ala	Thr		
225				230					235						240		
gcg	ctg	tgc	acg	gag	ctc	tgc	gac	aac	ctg	atc	gcg	ggc	ggg	gtg	gag	768	
Ala	Leu	Cys	Thr	Glu	Leu	Cys	Asp	Asn	Leu	Ile	Ala	Gly	Gly	Val	Glu		
			245					250						255			
gat	ctg	cat	ttc	tac	acg	ctg	aac	cgg	ccg	cag	atg	acc	cgc	gat	gtc	816	
Asp	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Pro	Gln	Met	Thr	Arg	Asp	Val		
		260					265					270					
tgc	cat	gcg	ctg	ggc	gtc	aac	ccg	ggt	gtg	gtg	ctg	gaa	aac	gtc	gcc	864	
Cys	His	Ala	Leu	Gly	Val	Asn	Pro	Gly	Val	Val	Leu	Glu	Asn	Val	Ala		
	275					280					285						
tga																867	

<210> 44

<211> 288

<212> PRT

<213> Rhodobacter

<400> 44

Met	Thr	Thr	Pro	His	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	Gln	Thr	Leu
1				5				10					15		

Asp	Ala	Ser	Phe	Arg	Leu	Trp	Glu	Thr	Ala	Gln	Val	Leu	Ala	Pro	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20					25					30					
Lys	Pro	Gly	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Gly	Gly	Thr	Thr	Arg
		35					40					45			
Lys	Leu	Thr	His	Glu	Ala	Val	Ala	Ala	Ile	His	Lys	Asn	Tyr	Gly	Leu
	50					55					60				
Asn	Val	Ala	Ala	His	Leu	Thr	Cys	Val	Asp	Ala	Thr	Arg	Ala	Glu	Thr
	65					70					75				80
Gln	Glu	Ile	Ile	Asp	Ala	Tyr	Ala	Glu	Ala	Gly	Val	Thr	Glu	Ile	Val
				85					90					95	
Ala	Leu	Arg	Gly	Asp	Pro	Pro	Lys	Gly	Ala	Ala	Arg	Phe	Thr	Pro	His
			100					105					110		
Pro	Asp	Gly	Phe	Ala	Ser	Ser	Val	Asp	Leu	Ile	Glu	Trp	Leu	Ala	Arg
		115					120					125			
Asp	Gly	Arg	Phe	Thr	Leu	Arg	Cys	Gly	Ala	Tyr	Pro	Glu	Pro	His	Pro
	130					135					140				
Glu	Ala	Ala	Asp	Thr	Leu	Ala	Asp	Val	Arg	Trp	Leu	Lys	Arg	Lys	Cys
	145					150					155				160
Glu	Ala	Gly	Ala	Thr	Ser	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Glu	Ala	Glu
				165					170					175	
Thr	Phe	Phe	Arg	Phe	Arg	Asp	Ala	Cys	Val	Lys	Glu	Gly	Ile	Thr	Ala
			180					185					190		
Lys	Ile	Ile	Pro	Gly	Ile	Leu	Pro	Ile	Gln	Ser	Trp	Lys	Gly	Ala	Lys
		195					200					205			
Ser	Phe	Ala	Gln	Arg	Cys	Gly	Thr	Ser	Ile	Pro	Thr	Trp	Val	Glu	Glu
		210					215					220			
Ala	Phe	Asp	His	Ala	Ile	Arg	Asp	Asp	Arg	Glu	Gln	Leu	Leu	Ala	Thr
				225		230					235				240
Ala	Leu	Cys	Thr	Glu	Leu	Cys	Asp	Asn	Leu	Ile	Ala	Gly	Gly	Val	Glu
				245					250					255	
Asp	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Pro	Gln	Met	Thr	Arg	Asp	Val
			260					265					270		
Cys	His	Ala	Leu	Gly	Val	Asn	Pro	Gly	Val	Val	Leu	Glu	Asn	Val	Ala
			275					280					285		

<210> 45

<211> 879

<212> DNA

<213> Neisseria meningitidis ser. A

<220>

<221> CDS

<222> (1)..(876)

<223> RNM00812

<400> 45

atg aat tac gca aaa gaa atc aat gcg tta aat aac agc ctt tcc gat	48
Met Asn Tyr Ala Lys Glu Ile Asn Ala Leu Asn Asn Ser Leu Ser Asp	
1 5 10 15	
ttg aaa ggc gac atc aac gtt tcg ttt gaa ttt ttt cca ccg aaa aac	96
Leu Lys Gly Asp Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn	
20 25 30	
gag caa atg gaa acg atg ctg tgg gat tcc atc cac cgt ctg caa acc	144
Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr	
35 40 45	
ctg cat ccc aag ttc gta tcc gta acc tac ggc gca aac tcc ggc gaa	192
Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
cgc gac cgc acg cac ggc atc gtc aaa cgc atc aaa cag gaa acc ggc	240
Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly	
65 70 75 80	
ttg gaa gca gca ccg cac ctg acc ggc atc gac gca tcc ccc gac gaa	288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu	
85 90 95	
ttg cgc caa atc gcc aaa gac tat tgg gac agc ggc atc cgc cgc att	336
Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
gtc gcc ctg cgt ggc gac gag ccg ccc ggt tat gag aaa aaa ccg ttt	384
Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe	
115 120 125	
tac gcc gaa gac ttg gtt aag cta tta cgc tcc gtc gcc gac ttc gac	432
Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp	
130 135 140	
atc tct gtg gcg gca tat ccc gaa gtg cat ccc gaa gcc aaa tcc gca	480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
caa gcc gat ctg att aat ctg aag cgc aaa atc gat gcg ggt gca aac	528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	
cac gtc atc acc caa ttt ttc ttt gac gta gaa cgc tac ctg cgc ttc	576
His Val Ile Thr Gln Phe Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe	
180 185 190	
cgc gac cgc tgc gtg atg ttg ggt atc gat gtg gaa atc gtc cct ggt	624
Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly	
195 200 205	
att ttg cct gtt acc aac ttc aag cag ctc ggc aaa atg gcg caa gta	672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val	
210 215 220	

acc aac gtc aaa atc cca agc tgg ctg tcg caa atg tat gaa ggt ttg 720
 Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu
 225 230 235 240

gac gac gac caa ggc acg cgc aac ctc gtc gcc gcc agt atc gcc atc 768
 Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile
 245 250 255

gat atg gtc aaa gtc ctg tcc cgc gaa ggc gtg aaa gat ttc cac ttc 816
 Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270

tac acg ctc aac cgc agc gag ctg act tac gcc atc tgc cat att tta 864
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Ile Leu
 275 280 285

ggc gtg cgc cct taa 879
 Gly Val Arg Pro
 290

<210> 46
 <211> 292
 <212> PRT
 <213> Neisseria meningitidis ser. A

<400> 46
 Met Asn Tyr Ala Lys Glu Ile Asn Ala Leu Asn Asn Ser Leu Ser Asp
 1 5 10 15

Leu Lys Gly Asp Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn
 20 25 30

Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr
 35 40 45

Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60

Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu
 85 90 95

Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe
 115 120 125

Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe
180 185 190

Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly
195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val
210 215 220

Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu
225 230 235 240

Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile
245 250 255

Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
260 265 270

Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Ile Leu
275 280 285

Gly Val Arg Pro
290

<210> 47

<211> 849

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(846)

<223> RCJ02911

<400> 47

atg tgt agt ttt tct ttt gaa gtt ttt cca cca aga aag gat gaa aat 48
Met Cys Ser Phe Ser Phe Glu Val Phe Pro Pro Arg Lys Asp Glu Asn
1 5 10 15

atc aaa aat ctt cat gct atc tta gat gat tta ggg caa tta agc cct 96
Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro
20 25 30

aat ttt atc agc gta acc ttt gga gct gga ggc tct att aac tca caa 144
Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln
35 40 45

aat act tta gaa gtt gca agc tta atc cag gaa gaa tat caa att cct 192
Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro
50 55 60

agc ata gta cat tta cct tgc atc cat tct agt aaa gaa aaa atc act 240
Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr
65 70 75 80

cag ata ctt caa aaa tgc aaa gaa aaa aat ctt aat caa att ctt gcc 288
Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala

85	90	95	
cta aga ggc gat ata tgt gaa aat tta aaa aaa agc aaa gat ttt tct Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser 100 105 110			336
tat gct agt gat tta att tct ttt ata aaa aaa caa gaa tac ttt gaa Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu 115 120 125			384
att tat gcc gca tgc tat ccc gaa aaa cat aat gaa tct aaa aat ttc Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe 130 135 140			432
atc gag gat ata cac cat ctt aaa act aag gta aat gca gga aca gat Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp 145 150 155 160			480
aag ctc att act caa ctt ttt tac gat aat gaa gat ttt tat act ttt Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe 165 170 175			528
aaa caa aat tgt gct tta gca gat att gac ata cct att tac gca ggt Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly 180 185 190			576
att atg cct att act aac aaa aga cag gtt tta aaa att tct caa ctt Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu 195 200 205			624
tgc gga gct aaa atc cct cct aaa ttt gtt aaa att tta gaa aaa tat Cys Gly Ala Lys Ile Pro Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr 210 215 220			672
gaa aat aat act ttg got tta gaa gat gca ggt atc gcg tat gct tgc Glu Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys 225 230 235 240			720
gat caa att gtc gat tta atc aca agt ggt gta gat gga att cat ctt Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu 245 250 255			768
tat act atg aat aaa tcc aaa gcg gct att aaa att tat gaa gct gta Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val 260 265 270			816
aag cat ttg ctt aaa gaa gag ctt cat gct tag Lys His Leu Leu Lys Glu Glu Leu His Ala 275 280			849

<210> 48

<211> 282

<212> PRT

<213> Campylobacter jejuni

<400> 48

Met	Cys	Ser	Phe	Ser	Phe	Glu	Val	Phe	Pro	Pro	Arg	Lys	Asp	Glu	Asn
1					5				10					15	

Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro
 20 25 30
 Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln
 35 40 45
 Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro
 50 55 60
 Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr
 65 70 75 80
 Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala
 85 90 95
 Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser
 100 105 110
 Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu
 115 120 125
 Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe
 130 135 140
 Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp
 145 150 155 160
 Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe
 165 170 175
 Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly
 180 185 190
 Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu
 195 200 205
 Cys Gly Ala Lys Ile Pro Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr
 210 215 220
 Glu Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys
 225 230 235 240
 Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu
 245 250 255
 Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val
 260 265 270
 Lys His Leu Leu Lys Glu Glu Leu His Ala
 275 280

<210> 49

<211> 852

<212> DNA

<213> Lactococcus lactis

<220>

<221> CDS

<222> (1)..(849)

<223> AAK05352

<400> 49

atg aca agt aat tcc aaa att ctt tct ttt gaa gtt ttt cca cct aca	48
Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr	
1 5 10 15	
act caa att gga agt acc aac ttg gta aag acc ttg gat agc cta aga	96
Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg	
20 25 30	
act ctc tcg cca gat ttt atc agt gta act tgt agt aac aat aat tat	144
Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr	
35 40 45	
gat aat att gga gat aca act ata aag ttt gct gat tat gta aac aat	192
Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn	
50 55 60	
aca cta gat att cca gcg gtt gct cat tta cct gcc gct tat tta gat	240
Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp	
65 70 75 80	
aaa gct caa gtg atc gaa att ttg gaa cgg tta aaa gat aaa caa atc	288
Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile	
85 90 95	
aaa aaa att ctt gct tta aga ggt gat atc agc gat gaa ccg atg aaa	336
Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys	
100 105 110	
gat gat ttt aaa ttt gca agt gat ttg gtt aaa ttt atc aaa gat tat	384
Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr	
115 120 125	
gat gat agt ttt gaa gtt tta ggt gct tgc tac ccc gat att cat ccc	432
Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro	
130 135 140	
gaa tca gta aat cga gtg agt gat ttt cat tat ctg aaa gaa aaa gta	480
Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val	
145 150 155 160	
gat gct ggt tgt gac aga tta atc acg caa cta ttt ttt gat aat gat	528
Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp	
165 170 175	
agt ttc tat gat ttt caa gaa cga tgc gca att gct gag ata aat act	576
Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr	
180 185 190	
ccg ata ttc gcc gga ata atg cca gta atc aat cga aat caa att ctt	624
Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu	
195 200 205	
cgt cta tta aaa aat tgt aat acg cca tta cca gca aaa ttc att aga	672
Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg	
210 215 220	
ata ctc gaa aaa tat gaa cat aat ctt atc gct tta agg gat gct gga	720

Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly
 225 230 235 240

att gct tac gcc atc gat caa atc gtt gat tta gta aca gag gat gtt 768
 Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val
 245 250 255

gct gga att cac ctc tat acg atg aat aat gca aat acg gca cac tcc 816
 Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser
 260 265 270

atc cat gct tca att tct tct tta ttt acc ttt tga 852
 Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe
 275 280

<210> 50

<211> 283

<212> PRT

<213> Lactococcus lactis

<400> 50

Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr
 1 5 10 15

Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg
 20 25 30

Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr
 35 40 45

Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn
 50 55 60

Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp
 65 70 75 80

Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile
 85 90 95

Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys
 100 105 110

Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr
 115 120 125

Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro
 130 135 140

Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val
 145 150 155 160

Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp
 165 170 175

Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr
 180 185 190

Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu

195	200	205
Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg 210 215 220		
Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly 225 230 235 240		
Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val 245 250 255		
Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser 260 265 270		
Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe 275 280		

<210> 51
 <211> 891
 <212> DNA
 <213> Prochlorococcus maritima

<220>
 <221> CDS
 <222> (1)..(888)
 <223> RCK01602

<400> 51	
ttg aaa tca aaa ctt cag caa act tta gaa aag aat tca aaa gta att Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile 1 5 10 15	48
aca gca gaa tta atg ccg cca aga gga gga gac ccc gta aga tct ctt Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu 20 25 30	96
aaa ata gca caa ctc ttg aga aat aag gtg cat gca gtt aat att aca Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr 35 40 45	144
gac gga agt aga gca ata atg aga atg tgt agt tta gca atg tct aaa Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys 50 55 60	192
cta tta cta gac aat ggg ata gaa cct ata atg cag atc tca tgt aga Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg 65 70 75 80	240
gat cgt aat aaa att gct tta caa tca gat att ctt gga gca aat gcc Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala 85 90 95	288
tta gga att aaa aat att tta tgc att aca gga gat tct gta aaa gcc Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala 100 105 110	336
gga gat cag caa gaa aca aaa gcc gtt cat gaa ttt gag gca gta aga Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg 115 120 125	384

tta tta aaa caa att caa tca ttc aat caa gga att gat cct act ttt 432
 Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
 130 135 140

gaa caa ctt cca gac aaa agg act gaa att ttc tca ggt gcg gca gta 480
 Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
 145 150 155 160

gat cca agt tgt cga aat caa aga agt tta aaa agt aga aca att aaa 528
 Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
 165 170 175

aaa aaa gag gcc ggt gca aat ttc tta caa act caa ata gtt atg gat 576
 Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
 180 185 190

aga aaa tgt tta gca gac ttt tgc aac gaa atc agt aat cca ctt gag 624
 Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
 195 200 205

ata cca gtt att gca gga gta ttt ctt tta aaa tca tat aaa aat gct 672
 Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
 210 215 220

ctt ttc ata aat aaa ttt gta cct gga gcg aat att cct gaa aat gtt 720
 Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
 225 230 235 240

tta aat cgt ctc aaa gat gca aaa aat cca ctt caa gaa gga ata tta 768
 Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255

att gct tca gag caa gct caa gat ttt att aat att gca gat gga att 816
 Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270

cat ctt atg gca gtc aaa tca gaa cat ctt atc cca gag ata ctt gaa 864
 His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285

aaa gct ggt ctc aat ctg gaa tgt taa 891
 Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 52

<211> 296

<212> PRT

<213> *Prochlorococcus maritima*

<400> 52

Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile
 1 5 10 15

Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu
 20 25 30

Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr
 35 40 45

Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys
 50 55 60
 Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg
 65 70 75 80
 Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala
 85 90 95
 Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala
 100 105 110
 Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg
 115 120 125
 Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
 130 135 140
 Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
 145 150 155 160
 Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
 165 170 175
 Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
 180 185 190
 Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
 195 200 205
 Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
 210 215 220
 Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
 225 230 235 240
 Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255
 Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270
 His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285
 Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 53

<211> 1848

<212> DNA

<213> *Bacillus stearothermophilus*

<220>

<221> CDS

<222> (1) .. (1845)

<223> RBE04103

<400> 53

gtg gga ttg ctg gat gag ttg aaa gag cgc att ctc atc gcc gac ggg	48
Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly	
1 5 10 15	
gcg atg gga acg ctt tta tat tgc cac ggc att gac cgt tgt ttt gaa	96
Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu	
20 25 30	
gaa ttg aat cta tcc aat cca gat gaa atc gtc cat att cat gaa gcg	144
Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala	
35 40 45	
tat atc gcc gcg ggc gcc gac gtc att cag acg aat aca tac ggc gcc	192
Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala	
50 55 60	
aac tat gtg aaa ctc gcc cgc tac ggc ctt gaa gat gag gtg ccg gcc	240
Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala	
65 70 75 80	
atc aac cgc gcg gcg gtg cgg ctc gcc agg caa gcg gcg aac gga cgg	288
Ile Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg	
85 90 95	
gca tac gtg ctc ggg acg atc ggg ggg ctg cgc acg tta aac aaa agc	336
Ala Tyr Val Leu Gly Thr Ile Gly Gly Leu Arg Thr Leu Asn Lys Ser	
100 105 110	
gtc gtc acg ctc gaa gaa gtg aag cgg acg ttt cgc gag cag ctg ttt	384
Val Val Thr Leu Glu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe	
115 120 125	
gtc ctg ctc gct gaa ggg gtc gac ggc gtg ctg ctc gag acg tat tac	432
Val Leu Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr	
130 135 140	
gat ttg gaa gag ttg gag acg gtg ctt gcc atc gcc cgc aaa gag acc	480
Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr	
145 150 155 160	
gac ttg ccg att atc gct cac gtc tgc ctc cat gaa gtc ggc gtc ttg	528
Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu	
165 170 175	
caa gat ggc acg ccg ctc gcg gac gcc ctt gcc cgc cta gag gcg ctc	576
Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu	
180 185 190	
ggg gcc gat gtc gtc gga ctg aac tgt cgt ctc ggt cca tat cat atg	624
Gly Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met	
195 200 205	
ctt cgg tgc ctc gag gaa gtg ccg ctg cca aat cga gcg ttt ttg tgc	672
Leu Arg Ser Leu Glu Glu Val Pro Leu Pro Asn Arg Ala Phe Leu Ser	
210 215 220	
gcg tat ccg aac gcc agc ctt ccg gat tac cgc gat ggg ccg ctt gtc	720
Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val	

225	230	235	240	
tat gag acg aac gct gaa tat ttc gag gaa acg gcc aaa gcg ttc cgc				768
Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg				
245	250	255		
gac caa ggg gtg cgc ttg atc ggc ggg tgc tgc ggc acg acg ccg aaa				816
Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys				
260	265	270		
cat atc gaa gcg atg gca aaa gcg ctc tcc gac cga acg ccg gtg acg				864
His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr				
275	280	285		
gaa aaa acg gtg aaa cgg cgc gcg gtg tct gta tca gtg caa gcg gag				912
Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu				
290	295	300		
cgg ccc gcc cca tct ccc ctt ccc gag ctt gcc cgc acg cac cgc tcg				960
Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser				
305	310	315	320	
gtc att gtg gag ctg gat ccg ccg aaa aaa ttg ggg att gac aag ttt				1008
Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe				
325	330	335		
ctt gcc ggg gcg aaa gcg ctc cat gac gcc ggc atc gat gcg ctg acg				1056
Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr				
340	345	350		
ttg gcc gac aac tcg ctc gcc acg ccg cgc atc agc aac gcc gct gtc				1104
Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val				
355	360	365		
gcc acg atc atc aag gag caa ctc ggc atc cgc ccg ctc gtg cat att				1152
Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile				
370	375	380		
aca tgc cgc gat cgc aat ttg atc ggc ttg cag tcg cat ttg atg ggc				1200
Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly				
385	390	395	400	
ttg cat acg ctc ggc atc acc gat gtg ctc gcc att acc ggc gac ccg				1248
Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro				
405	410	415		
tcg aaa atc ggc gat ttt cca ggg gca acg tcc gtg tac gac tta tca				1296
Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser				
420	425	430		
tcg ttc gat ttg atc cgc ttg atc cgc cag ttt aac gaa ggg ctg tcg				1344
Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser				
435	440	445		
tac tcg ggc aaa ccg ctt ggg caa aaa acg aac ttc tcg atc ggc gct				1392
Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala				
450	455	460		
gcg ttc aac ccg aac gtc cgc cat ttg gac aaa gcg gtc gag ccg atg				1440
Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met				

465	470	475	480	
gag aaa aaa atc caa tgc ggc gcc cat tat ttc ttg acc cag ccg att				1488
Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile				
485		490	495	
tac tcg gaa gag aaa atc gtt gaa gtg cac gaa gcg acc aag cat ctt				1536
Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu				
500		505	510	
gac acg ccg att tac atc ggc att atg ccg ctt gtg agc gcg cgc aac				1584
Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn				
515		520	525	
gcc gac ttt ttg cat cat gaa gtg ccg ggc att acg ctc tct gac gag				1632
Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu				
530		535	540	
att cgc gcc cgc atg gcc gcc tgc agc ggc gac ccg gtg caa gca gcc				1680
Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala				
545		550	555	560
aag gaa ggc atc gct atc gcc aaa tcg ctc att gac gct gcg ttt gat				1728
Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp				
565		570	575	
ttg ttt aac ggc att tat ttg atc acg ccg ttc ttg cgc tac gac atg				1776
Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met				
580		585	590	
acg gtc gag ctt gtc cgc tac att cac gaa aaa gaa gcg gcc gcc aaa				1824
Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys				
595		600	605	
gaa agg aag gtt gtt cat ggc taa				1848
Glu Arg Lys Val Val His Gly				
610		615		
 <210> 54				
<211> 615				
<212> PRT				
<213> Bacillus stearothermophilus				
 <400> 54				
Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly				
1		5	10	15
Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu				
	20		25	30
Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala				
	35		40	45
Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala				
	50		55	60
Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala				
	65		70	75
				80

Ile	Asn	Arg	Ala	Ala	Val	Arg	Leu	Ala	Arg	Gln	Ala	Ala	Asn	Gly	Arg	85	90	95
Ala	Tyr	Val	Leu	Gly	Thr	Ile	Gly	Gly	Leu	Arg	Thr	Leu	Asn	Lys	Ser	100	105	110
Val	Val	Thr	Leu	Glu	Glu	Val	Lys	Arg	Thr	Phe	Arg	Glu	Gln	Leu	Phe	115	120	125
Val	Leu	Leu	Ala	Glu	Gly	Val	Asp	Gly	Val	Leu	Leu	Glu	Thr	Tyr	Tyr	130	135	140
Asp	Leu	Glu	Glu	Leu	Glu	Thr	Val	Leu	Ala	Ile	Ala	Arg	Lys	Glu	Thr	145	150	155
Asp	Leu	Pro	Ile	Ile	Ala	His	Val	Ser	Leu	His	Glu	Val	Gly	Val	Leu	165	170	175
Gln	Asp	Gly	Thr	Pro	Leu	Ala	Asp	Ala	Leu	Ala	Arg	Leu	Glu	Ala	Leu	180	185	190
Gly	Ala	Asp	Val	Val	Gly	Leu	Asn	Cys	Arg	Leu	Gly	Pro	Tyr	His	Met	195	200	205
Leu	Arg	Ser	Leu	Glu	Glu	Val	Pro	Leu	Pro	Asn	Arg	Ala	Phe	Leu	Ser	210	215	220
Ala	Tyr	Pro	Asn	Ala	Ser	Leu	Pro	Asp	Tyr	Arg	Asp	Gly	Arg	Leu	Val	225	230	235
Tyr	Glu	Thr	Asn	Ala	Glu	Tyr	Phe	Glu	Glu	Thr	Ala	Lys	Ala	Phe	Arg	245	250	255
Asp	Gln	Gly	Val	Arg	Leu	Ile	Gly	Gly	Cys	Cys	Gly	Thr	Thr	Pro	Lys	260	265	270
His	Ile	Glu	Ala	Met	Ala	Lys	Ala	Leu	Ser	Asp	Arg	Thr	Pro	Val	Thr	275	280	285
Glu	Lys	Thr	Val	Lys	Arg	Arg	Ala	Val	Ser	Val	Ser	Val	Gln	Ala	Glu	290	295	300
Arg	Pro	Ala	Pro	Ser	Pro	Leu	Pro	Glu	Leu	Ala	Arg	Thr	His	Arg	Ser	305	310	315
Val	Ile	Val	Glu	Leu	Asp	Pro	Pro	Lys	Lys	Leu	Gly	Ile	Asp	Lys	Phe	325	330	335
Leu	Ala	Gly	Ala	Lys	Ala	Leu	His	Asp	Ala	Gly	Ile	Asp	Ala	Leu	Thr	340	345	350
Leu	Ala	Asp	Asn	Ser	Leu	Ala	Thr	Pro	Arg	Ile	Ser	Asn	Ala	Ala	Val	355	360	365
Ala	Thr	Ile	Ile	Lys	Glu	Gln	Leu	Gly	Ile	Arg	Pro	Leu	Val	His	Ile	370	375	380
Thr	Cys	Arg	Asp	Arg	Asn	Leu	Ile	Gly	Leu	Gln	Ser	His	Leu	Met	Gly	385	390	395

Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro
 405 410 415
 Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser
 420 425 430
 Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser
 435 440 445
 Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala
 450 455 460
 Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met
 465 470 475 480
 Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile
 485 490 495
 Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu
 500 505 510
 Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn
 515 520 525
 Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu
 530 535 540
 Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala
 545 550 555 560
 Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp
 565 570 575
 Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met
 580 585 590
 Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys
 595 600 605
 Glu Arg Lys Val Val His Gly
 610 615

<210> 55

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 55

cccggtgatcc gctagcggcg cgccggccgg cccggtgtga aataccgcac ag

52

<210> 56

<211> 53

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 56

tctagactcg agcggccgcg gccggccttt aaattgaaga cgaaagggcc tcg 53

<210> 57

<211> 47

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 57

gagatctaga cccggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 58

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 58

gagaggcgcg ccgctagcgt gggcgaagaa ctccagca 38

<210> 59

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 59

gagagggcgg ccgcgcaaag tcccgttcg tgaa 34

<210> 60

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 60

gagagggcgg ccgctcaagt cggctcaagcc acgc 34

<210> 61

<211> 140

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 61

```
tcgaatttaa atctcgagag gcctgacgtc gggcccggta ccacgcgtca tatgactagt 60
tcggacctag ggatatcgtc gacatcgatg ctcttctgcg ttaattaaca attgggatcc 120
tctagaccgc ggatttaaatt                                     140
```

<210> 62

<211> 140

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 62

```
gatcatttaa atcccgggtc tagaggatcc caattgttaa ttaacgcaga agagcatcga 60
tgtcgacgat atccctaggt ccgaactagt catatgacgc gtggtaccgg gcccgacgtc 120
aggcctctcg agatttaaatt                                     140
```

<210> 63

<211> 33

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 63

```
gagagcggcc gccgacctt ttttaacccat cac                                     33
```

<210> 64

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 64

```
aggagcggcc gccatcggca ttttcttttg cg                                     32
```

<210> 65

<211> 5091

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:plasmid

<400> 65

```
gccgcgactg ctttcgcgaa gccttgcccc gcggaaattt cctccaccga gttcgtgcac 60
accctatgc caagcttctt tcaccctaaa ttcgagagat tggattctta ccgtggaaat 120
tcttcgcaaa aatcgcccc tgatcgccct tgcgacgttg gcgtcggtgc cgctggttgc 180
```

gcttggttg accgacttga tcagcgggccg ctcgatttaa atctcgagag gcctgacgtc 240
gggcccgtga ccacgcgtca tatgactagt tcggacctag ggatatcgtc gacatcgatg 300
ctcttctgcg ttaattaaca attgggatcc tctagaccgg ggattttaa atcgctagcggg 360
ctgctaaaagg aagcggaaca cgtagaaaagc cagtccgcag aaacgggtgct gaccccggt 420
gaatgtcagc tactgggcta tctggacaag ggaaaaacgca agcgcaaaga gaaagcaggt 480
agcttgacgt gggcttacat ggcgatagct agactgggag gttttatgga cagcaagcga 540
accggaattg ccagctgggg cgccctctgg taagggtggg aagccctgca aagtaaaactg 600
gatggctttc ttgccgcaa ggatctgatg gcgcagggga tcaagatctg atcaagagac 660
aggatgagga tcgtttcgca tgattgaaca agatggattg cacgcaggtt ctccggccgc 720
ttgggtggag aggctattcg gctatgactg ggcacaacag acaatcggct gctctgatgc 780
cgccgtgttc cggctgtcag cgcaggggag cccggttctt tttgtcaaga ccgacctgtc 840
cgggtgccctg aatgaactgc aggacgaggc agcgcggtta tcgtgggtgg ccacgacggg 900
cgttccttgc gcagctgtgc tcgacgttgt cactgaagcg ggaagggact ggctgctatt 960
gggcgaagtg ccggggcagg atctcctgtc atctcacctt gctcctgccg agaaagtatc 1020
catcatggct gatgcaatgc ggcggtgca tacgcttgat ccggctacct gccattcga 1080
ccaccaagcg aaacatcgca tcgagcgagc acgtactcgg atggaagccg gtcttgtcga 1140
tcaggatgat ctggacgaag agcatcaggg gctcgcgcca gccgaactgt tcgccaggct 1200
caaggcgcg atgcccagc gcgaggatct cgtcgtgacc catggcgatg cctgcttgcc 1260
gaatatcatg gtggaaaatg gccgcttttc tggattcatc gactgtggcc ggctgggtgt 1320
ggcggagcgc tatcaggaca tagcgttggc taccgctgat attgctgaag agcttggcgg 1380
cgaatgggct gaccgcttcc tcgtgcttta cggtatcgcc gctcccgaat cgcagcgcat 1440
cgcttctat cgcttcttgc acgagttctt ctgagcgga ctctgggtt cgaaatgacc 1500
gaccaagcga cgcccaacct gccatcacga gatttcgatt ccaccgccc cttctatgaa 1560
aggttgggct tcggaatcgt tttccgggac gccggtgga tgatcctcca gcgcggggat 1620
ctcatgctgg agttcttcgc ccacgctagc ggcgcgccgg ccggcccgg gtgaaatacc 1680
gcacagatgc gtaaggagaa aataccgcat caggcgctct tccgcttct cgtcactga 1740
ctcgtcgcgc tcggctcgttc ggctgcggcg agcggtatca gctcactcaa aggcggtaat 1800
acggttatcc acagaatcag gggataacgc aggaagaac atgtgagcaa aaggccagca 1860
aaaggccagg aaccgtaaaa aggcgcggt gctggcggtt tccataggc tccgcccccc 1920
tgacgagcat caaaaaatc gacgctcaag tcagaggtgg cgaaaccga caggactata 1980
aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc cgaccctgcc 2040
gcttaccgga tacctgtccg cctttctccc ttcgggaagc gtggcgcttt ctcatagctc 2100
acgtgtagg tatctcagtt cgggtgtagt cgttcgctcc aagctgggct gtgtgcacga 2160
acccccggt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg agtccaacc 2220
ggtaagacac gacttatcgc cactggcagc agccactggt aacaggatta gcagagcgag 2280
gtatgtaggc ggtgtacag agttcttgaa gtgggtggcc aactacggct acactagaag 2340
gacagtattt ggtatctgcg ctctgctgaa gccacttacc ttcggaaaaa gagtgggtga 2400
ctcttgatcc ggcaaacaaa ccaccgctgg tagcgggtgt tttttgtt gcaagcagca 2460
gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta cggggtctga 2520
cgctcagtg aacgaaaact cacgttaagg gattttggtc atgagattat caaaaaggat 2580
cttcacctag atccttttaa aggcgggccc cggcgcgca aagtcgct tcgtgaaaat 2640
tttctgccc cgtgattttc cgcaaaaaac tttacgaac gttcgttata atggtgtcat 2700
gaccttcacg acgaagtact aaaattggcc cgaatcatca gctatggatc tctctgatgt 2760
cgcgctggag tccgacgcgc tcgatgctgc cgtcgattta aaaacgggtga tcggattttt 2820
ccgagctctc gatacgacgg acgcgccagc atcacgagac tgggcccagtg ccgcgagcga 2880
cctagaaact ctcgtggcgg atcttgagga gctggctgac gagctgcgtg ctcgccagc 2940
gccaggagga cgcacagtag tggaggatgc aatcagttgc gcctactgcg gtggcctgat 3000
tctccccgg cctgaccgcg gaggacggcg cgcaaaatat tgctcagatg cgtgtcgtgc 3060
cgcagccagc cgcgagcgcg ccaacaaacg ccacgccgag gagctggagg cggctaggtc 3120
gcaaatggcg ctggaagtgc gtcccccgag cgaaattttg gccatggctg tcacagagct 3180
ggaagcggca gcgagaatta tcgcatcgt ggcggtgccc gcaggcatga caaacatcgt 3240
aaatgcccgc tttcgtgtgc cgtggccgccc caggacgtgt cagcgccgccc accacctgca 3300
ccgaatcggc agcagcgtcg cgcgtcgaaa aagcgcacag gcggcaagaa gcgataagct 3360
gcacgaatac ctgaaaaatg ttgaacgccc cgtgagcggc aactcacagg gcgtcggcta 3420
acccccagtc caaacctggg agaaagcgct caaaaatgac tctagcggat tcacgagaca 3480
ttgacacacc ggcctggaaa ttttcgctg atctgttcga caccatccc gagctcgcgc 3540
tgcatcacg ttgctggagc agcgaagacc gccgcgaatt cctcgtcac ctgggcagag 3600
aaaatttcca ggcagcaag accgcgact tcgccagcgc ttggatcaaa gaccgggaca 3660
cggagaaaca cagccgaagt tataccgagt tggttcaaaa tcgcttgcgc ggtgccagta 3720
tggtgtctg acgcagcgc agcagcagc cgtgcttgtc ctggacattg atgtgccgag 3780

```

ccaccaggcc ggcgggaaaa tcgagcacgt aaaccccgag gtctacgcga ttttggagcg 3840
ctgggcacgc ctggaaaaaag cgccagcttg gatcggcggtg aatccactga gcgggaaatg 3900
ccagctcatc tgggtcattg atccggtgta tgccgcagca ggcatgagca gcccgaatat 3960
gcgctgctg gctgcaacga ccgaggaaat gacccgcgtt ttcggcgctg accaggcttt 4020
ttcacatagg ctgagccgtg gccactgcac tctccgacga tcccagccgt accgctggca 4080
tgcccagcac aatcgcggtg atcgcttagc tgatcttatg gaggttgctc gcatgatctc 4140
aggcacagaa aaacctaataa aacgctatga gcaggagttt tctagcggac gggcacgtat 4200
cgaagcggca agaaaaagcca ctgcggaagc aaaagcactt gccacgcttg aagcaagcct 4260
gccgagcgcc gctgaagcgt ctggagagct gatcgacggc gtccgtgtcc tctggactgc 4320
tccagggcgt gccgcccgtg atgagacggc ttttcgccac gctttgactg tgggatacca 4380
gttaaaagcg gctggtgagc gcctaaaaga caccaagggt catcgagcct acgagcgtgc 4440
ctacaccgtc gctcaggcgg tcggaggagg ccgtgagcct gatctgccgc cggactgtga 4500
ccgccagacg gattggccgc gacgtgtgcg cggctacgtc gctaaaggcc agccagtcgt 4560
ccctgctcgt cagacagaga cgcagagcca gccgaggcga aaagctctgg ccactatggg 4620
aagacgtggc ggtaaaaaagg ccgcagaacg ctggaaaagc ccaaacagtg agtacgcccg 4680
agcacagcga gaaaaactag ctaagtccag tcaacgacaa gctaggaaaag ctaaaggaaa 4740
tcgcttgacc attgcaggtt ggtttatgac tgttgaggga gagactggct cgtggccgac 4800
aatcaatgaa gctatgtctg aatttagcgt gtcacgtcag accgtgaata gagcacttaa 4860
ggctgcggg cattgaactt ccacgaggac gccgaaagct tcccagtaaa tgtgccatct 4920
cgtaggcaga aaacgggttc ccgtaggggt ctctctcttg gcctcctttc taggtcgggc 4980
tgattgctct tgaagctctc tagggggggt cacaccatag gcagataacg ttccccaccg 5040
gctcgcctcg taagcgcaca aggactgctc ccaaagatct tcaaagccac t 5091

```

<210> 66

<211> 4323

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 66

```

tctctcagcg tatggttgct gcctgagctg tagttgcctt catcgatgaa ctgctgtaca 60
ttttgatagc tttttccgtc accgtcaaag attgatttat aatcctctac accgttgatg 120
ttcaaagagc tgtctgatgc tgatacgtta acttgctgag ttgtcagtg ttgtttgccg 180
taatgtttac cggagaaatc agtgtagaat aaacggattt ttcggtcaga tgtaaatgtg 240
gctgaacctg accattcttg tgtttggtct tttaggatag aatcatttgc atcgaatttg 300
tcgctgtctt taaagacgcg gccagcgttt ttccagctgt caatagaagt ttccgccgact 360
ttttgataga acatgtaaat cgatgtgtca tccgatttt taggatctcc ggctaatagca 420
aagacgatgt ggtagccgtg atagtttgcg acagtgcgt cagcgttttg taatggccag 480
ctgtcccaa cgtccaggcc ttttgacaga gagatatttt taattgtgga cgaatcaaat 540
tcagaaactt gatatttttc atttttttgc tgttcaggga tttgcagcat atcatggcgt 600
gtaatatggg aaatgccgta tgtttcctta tatggctttt gggttcgtttc tttcgcaaac 660
gcttgagttg cgcctcctgc cagcagtgcg gtagtaaagg ttaatactgt tgcttgtttt 720
gcaaactttt tgatgttcat cgttcattgc tcttttttta tgtactgtgt tagcgggtctg 780
cttcttccag cctcctgtgt tgaagatggc aagttagtta cgcacaataa aaaaagacct 840
aaaatatgta aggggtgacg ccaaagtata cactttgccc tttacacatt ttaggtcttg 900
cctgctttat cagtaacaaa ccgcgcgat ttacttttcg acctcattct attagactct 960
cgtttggatt gcaactggtc tattttcctc ttttgtttga tagaaaatca taaaaggatt 1020
tgcagactac gggcctaaag aactaaaaaa tctatctggt tcttttcatt ctctgtattt 1080
tttatagttt ctggtgcatg ggcataaagt tgccctttta atcacaattc agaaaatata 1140
ataatatctc atttctacta ataatagtga acggcaggta tatgtgatgg gttaaaaagg 1200
atcggcggcc gctcgattta aatctcgaga ggctgacgt cgggcccggg accacgcgtc 1260
atatgactag ttccgacctt gggatatcgt cgacatcgat gctcttctgc gtttaattac 1320
aattgggata ctctagacct gggattttaa tcgctagcgg gctgctaaag gaagcggaac 1380
acgtagaaag ccagtcgcga gaaacgggtg tgaccccgga tgaatgtcag ctactgggct 1440
atctggacaa gggaaaacgc aagcgcaaag agaaagcagg tagcttgtag tgggcttaca 1500
tggcgatagc tagactgggc ggtttttatg acagcaagcg aaccggaatt gccagctggg 1560

```



```

gcgcccctctg gtaagggttg gaagccctgc aaagtaaact ggatggcttt cttgccgcca 1620
aggatctgat ggcgcagggg atcaagatct gatcaagaga caggatgagg atcgtttcgc 1680
atgattgaac aagatggatt gcacgcaggt tctccggccg cttgggtgga gaggctattc 1740
ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt ccggctgtca 1800
gcgcaggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct gaatgaactg 1860
caggacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg cgcagctgtg 1920
ctcgacgttg tcaactgaagc gggaaaggac tggtgtctat tgggcgaagt gccggggcag 1980
gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc tgatgcaatg 2040
cggcggtctgc atacgcttga tccggctacc tgcccattcg accaccaagc gaaacatcgc 2100
atcgagcgag cacgtactcg gatggaagcc ggtcttgcg atcaggatga tctggacgaa 2160
gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgcg catgcccgcg 2220
ggcgaggatc tcgtcgtgac ccatggcgat gctcgttgc cgaatatcat ggtggaaaat 2280
ggccgctttt ctggattcat cgactgtggc cggtcgggtg tggcggaccg ctatcaggac 2340
atagcgttgg ctacccgtga tattgtgtaa gagcttggcg gcgaatgggc tgaccgcttc 2400
ctcgtgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta tcgccttctt 2460
gacgagttct tctgagcggg actctggggg tcgaaatgac cgaccaagcg acgcccacc 2520
tgccatcacg agatttcgat tccaccgccg ccttctatga aaggttgggc ttcggaatcg 2580
ttttccggga cgccggctgg atgatcctcc agcgcgggga tctcatgctg gagttcttcg 2640
cccacgctag cggcgcgccg gccggccccg tgtgaaatac cgcacagatg cgtaaggaga 2700
aaataccgca tcaggcgctc ttccgcttcc tcgctcactg actcgtcgcg ctcggtcgtt 2760
cggctgcggc gagcgggtat agctcactca aaggcggtaa tacggttatc cacagaatca 2820
ggggataacg caggaaagaa catgtgagca aaaggccagc aaaaggccag gaaccgtaaa 2880
aaggccgcgt tgctggcggt tttccatagg ctccgccccc ctgacgagca tcacaaaaat 2940
cgacgctcaa gtcagaggtg gcgaaacccg acaggactat aaagatacca ggcgtttccc 3000
cctggaagct cctcgtgcg ctctcctgtt ccgaccctgc cgcttacggg atacctgtcc 3060
gcctttctcc cttcggaag cgtggcgctt tctcatagct cacgctgtag gtatctcagt 3120
tcggtgtagg tcgttcgctc caagctgggc tgtgtgcacg aacccccgt tcagcccgcg 3180
cgctgcgcct tatccggtaa ctatcgtctt gagtccaacc cggtaaagaca cgacttatcg 3240
ccactggcag cagccactgg taacaggatt agcagagcga ggtatgtagg cggtgctaca 3300
gagttcttga agtggtggcc taactacggc tacactagaa ggacagtatt tggatatctg 3360
gctctgctga agccagttac cttcggaaaa agagttggta gctcttgatc cggcaaaaaa 3420
accaccgctg gtagcgggtg tttttttgtt tgcaagcagc agattacgcg cagaaaaaaa 3480
ggatctcaag aagatccttt gatcttttct acggggctct acgctcagtg gaacgaaaac 3540
tcacgttaag ggatttttgt catgagatta tcaaaaagga tcttcacctg gatcctttta 3600
aaggccggcc gcggccgcca tcggcatttt cttttgcgtt tttatttggt aactgttaat 3660
tgtccttggt caaggatgct gtctttgaca acagatgttt tcttgccctt gatgttcagc 3720
aggaagctcg gcgcaaactg tgattgtttg tctgcgtaga atcctctgtt tgtcatatag 3780
cttgtaatca cgacattgtt tcctttcgct tgaggtacag cgaagtgtga gtaagtaaag 3840
gttacatcgt taggatcaag atccattttt aacacaaggc cagttttgtt cagcggcttg 3900
tatgggccag ttaaagaatt agaaacataa ccaagcatgt aaatatcggt agacgtaatg 3960
ccgtcaatcg tcatttttga tccgcgggag tcagtgaaca ggtaccattt gccgttcatt 4020
ttaaagacgt tcgcgcgttc aatttcactt gttactgtgt tagatgcaat cagcggtttc 4080
atcacttttt tcagtgtgta atcatcgttt agctcaatca taccgagagc gccgtttgct 4140
aactcagccg tcgctttttt atcgctttgc agaagttttt gactttcttg acggaagaat 4200
gatgtgcttt tgccatagta tgctttgtta aataaagatt cttcgccttg gtagccatct 4260
tcagttccag tgtttgcttc aaataactaag tatttgtggc ctttatcttc tacgtagtga 4320
gga 4323

```

<210> 67

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 67

gagagagaga cgcggtcccag tggctgagac gcatc

35

<210> 68

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 68

ctctctctgt cgacgaattc aatcttacgg cctg

34

<210> 69

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 69

cccgggtacca cgcggtcccag tggctgagac gcatccgcta aagccccagg aaccctgtgc 60

agaaagaaaa cactcctctg gctaggtaga cacagtttat aaaggtagag ttgagcgggt 120

aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg 180

cggttcctcg cttgagagtg cggaacgcat tagaaacgtc gctgaacgga tcgttgccac 240

caagaaggct ggaaatgatg tcgtgggtgt ctgctccgca atgggagaca ccacggatga 300

acttctagaa cttgcagcgg cagtgaatcc cgttccgcca gctcgtgaaa tggatatgct 360

cctgactgct ggtgagcgta tttctaacgc tctcgtcgcc atggctattg agtcccttgg 420

cgcagaagcc caatctttca cgggctctca ggctgggtgtg ctcaccaccg agcgccacgg 480

aaacgcacgc attggtgatg tcaactccagg tcgtgtgcgt gaagcactcg atgagggcaa 540

gatctgcatt gttgctgggt tccaggggtg taataaagaa acccgcgatg tcaccacggt 600

gggtcgtggg ggttctgaca ccaactgcagt tgcgttggca gctgctttga acgctgatgt 660

gtgtgagatt tactcggacg ttgacggtgt gtataccgct gacccgcgca tcgttcctaa	720
tgcacagaag ctggaaaagc tcagcttcga agaaatgctg gaacttgctg ctgttggtc	780
caagattttg gtgctgcgca gtgttgaata cgctcgtgca ttcaatgtgc cacttcgcgt	840
acgtcgtct tatagtaatg atcccggcac tttgattgcc ggctctatgg aggatattcc	900
tgtggaagaa gcagtcctta ccggtgtcgc aaccgacaag tccgaagcca aagtaaccgt	960
tctgggtatt tccgataagc caggcgaggc tgcgaagggt ttccgtgcgt tggctgatgc	1020
agaaatcaac attgacatgg ttctgcagaa cgtctcttct gtagaagacg gcaccaccga	1080
catcaccttc acctgccctc gttccgacgg ccgccgcgcg atggagatct tgaagaagct	1140
tcaggttcag ggcaactgga ccaatgtgct ttacgacgac caggtcggca aagtctccct	1200
cgtgggtgct ggcatgaagt ctcacccagg tgttaccgca gagttcatgg aagctctgcg	1260
cgatgtcaac gtgaacatcg aattgatttc cacctctgag attcgtattt ccgtgctgat	1320
ccgtgaagat gatctggatg ctgctgcacg tgcattgcat gagcagttcc agctgggcgg	1380
cgaagacgaa gccgtcgttt atgcaggcac cggacgctaa agttttaaag gagtagtttt	1440
acaatgacca ccatcgcagt tggttggtgca accggccagg tcggccagggt tatgcgcacc	1500
cttttggaag agcgcaatth cccagctgac actgttcggt tctttgcttc cccacgttcc	1560
gcaggccgta agattgaatt cgtcgacatc gatgctcttc tgcgttaatt aacaattggg	1620
atcctctaga cccgggattt aaatcgctag cgggctgcta aaggaagcgg aacacgtaga	1680
aagccagtcc gcagaaacgg tgctgacccc ggatgaatgt cagctactgg gctatctgga	1740
caagggaaaa cgcaagcgca aagagaaagc aggtagcttg cagtgggctt acatggcgat	1800
agctagactg ggcggtttta tggacagcaa gcgaaccgga attgccagct ggggcgcct	1860
ctggtaaggt tgggaagccc tgcaaagtaa actggatggc tttcttgccg ccaaggatct	1920
gatggcgcag gggatcaaga tctgatcaag agacaggatg aggatcgttt cgcattgatg	1980
aacaagatgg attgcacgca ggttctccgg ccgcttgggt ggagaggcta ttcggctatg	2040
actgggcaca acagacaatc ggctgctctg atgccgccgt gttccggctg tcagcgcagg	2100
ggcgcccggt tctttttgtc aagaccgacc tgtccggtgc cctgaatgaa ctgcaggacg	2160
aggcagcgcg gctatcgtgg ctggccacga cgggcgttcc ttgcgcagct gtgctcgacg	2220
ttgtcactga agcgggaagg gactggctgc tattgggcga agtgccgggg caggatctcc	2280
tgtcatctca ccttgctcct gccgagaaag tatccatcat ggctgatgca atgcggcggc	2340
tgcatacgct tgatccggct acctgcccat tcgaccacca agcgaaacat cgcacgcagc	2400
gagcacgtac tcggatggaa gccggtcttg tcgatcagga tgatctggac gaagagcatc	2460

aggggctcgc gccagccgaa ctgttcgcca ggctcaaggc gcgcatgccc gacggcgagg	2520
atctcgtcgt gacccatggc gatgcctgct tgccgaatat catggtggaa aatggccgct	2580
tttctggatt catcgactgt ggccggctgg gtgtggcgga ccgctatcag gacatagcgt	2640
tggctacccg tgatattgct gaagagcttg gcggcgaaatg ggctgaccgc ttcctcgtgc	2700
tttacggtat cgccgctccc gattcgcagc gcacgcctt ctatgcctt cttgacgagt	2760
tcttctgagc gggactctgg ggttcgaaat gaccgaccaa gcgacgccc acctgccatc	2820
acgagatttc gattccaccg ccgccttcta tgaaaggttg ggcttcggaa tcgttttccg	2880
ggacgccggc tggatgatcc tccagcgcg ggatctcatg ctggagttct tcgcccacgc	2940
tagcggcgcg ccggccggcc cgggtgtgaaa taccgcacag atgcgtaagg agaaaatacc	3000
gcacagggcg ctcttccgct tctcgcctca ctgactcgtc gcgctcggtc gttcggctgc	3060
ggcgagcggc atcagctcac tcaaaggcgg taatacgggt atccacagaa tcaggggata	3120
acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg	3180
cgttgcctggc gtttttccat aggtccgcc ccctgacga gcacacaaa aatcgacgt	3240
caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcgttt cccctggaa	3300
gctccctcgt gcgctctcct gttccgacct tgccgcttac cggataacctg tccgccttcc	3360
tcccttcggg aagcgtggcg ctttctcata gctcacgtg taggtatctc agttcgggtg	3420
aggctcgttcg ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg	3480
ccttatccgg taactatcgt cttgagtcca acccggttaag acacgactta tcgccactgg	3540
cagcagccac tggtaacagg attagcagag cgaggatatgt aggcggtgct acagagttct	3600
tgaagtggcg gcctaactac ggctacacta gaaggacagt atttggatc tgcgctctgc	3660
tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg	3720
ctggtagcgg tggttttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc	3780
aagaagatcc tttgatcttt tctacggggc ctgacgctca gtggaacgaa aactcacgtt	3840
aagggtttt ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttaaaggccg	3900
gccgcggccg ccatcggcat tttcttttgc gtttttattt gttaactgtt aattgtcctt	3960
gttcaaggat gctgtctttg acaacagatg tttcttgcc tttgatgttc agcaggaagc	4020
tcggcgcaaa cgttgattgt ttgtctgcgt agaatcctct gtttgtcata tagcttgtaa	4080
tcacgacatt gtttccttcc gcttgaggta cagcgaagtg tgagtaagta aaggttacat	4140
cgttaggatc aagatccatt tttaacacaa ggccagtttt gttcagcggc ttgtatgggc	4200
cagttaaaga attagaaaca taaccaagca tgtaaataac gtttagacgta atgccgtcaa	4260

tcgtcatttt tgatccgcgg gagtcagtga acagggtacca tttgccgttc attttaaaga 4320
 cgttcgcgcg ttcaatttca tctgttactg tgtagatgc aatcagcggg ttcactcatt 4380
 ttttcagtgt gtaatcatcg ttttagctcaa tcataccgag agcgccgttt gctaactcag 4440
 ccgtgcgttt tttatcgctt tgcagaagtt tttgactttc ttgacggaag aatgatgtgc 4500
 ttttgccata gtatgctttg ttaaataaag attcttcgcc ttggtagcca tcttcagttc 4560
 cagtgtttgc ttcaaatact aagtatttgt ggcctttatc ttctacgtag tgaggatctc 4620
 tcagcgtatg gttgtcgctt gagctgtagt tgccttcacg gatgaactgc tgtacatttt 4680
 gatacgtttt tccgtcaccg tcaaagattg atttataatc ctctacaccg ttgatgttca 4740
 aagagctgtc tgatgctgat acgttaactt gtgcagttgt cagtgtttgt ttgccgtaat 4800
 gtttaccgga gaaatcagtg tagaataaac ggatttttcc gtcagatgta aatgtggctg 4860
 aacctgacca ttcttgtgtt tgggtcttta ggatagaatc atttgcatcg aatttgtcgc 4920
 tgtcttttaa gacggggcca gcgtttttcc agctgtcaat agaagtttcg ccgacttttt 4980
 gatagaacat gtaaatacgat gtgtcatccg catttttagg atctccggct aatgcaaaga 5040
 cgatgtggta gccgtgatag tttgcgacag tgccgtcagc gttttgtaat ggccagctgt 5100
 cccaaacgtc caggcctttt gcagaagaga tatttttaat tgtggacgaa tcaaattcag 5160
 aaacttgata tttttcattt ttttgcgtgt cagggatttg cagcatatca tggcgtgtaa 5220
 tatgggaaat gccgtatgtt tccttatatg gcttttggtt cgtttctttc gcaaacgctt 5280
 gagttgcgcc tcctgccagc agtgcggtag taaagggtta tactgttgct tgttttgcaa 5340
 actttttgat gttcatcggt catgtctcct ttttatgta ctgtgttagc ggtctgcttc 5400
 ttccagccct cctgtttgaa gatggcaagt tagttacgca caataaaaaa agacctaaaa 5460
 tatgtaaggg gtgacgcaa agtatacact ttgcccttta cacatttttag gtcttgctg 5520
 ctttatcagt aacaaacccg cgcgatttac ttttcgacct cattctatta gactctcggt 5580
 tggattgcaa ctgggtctatt ttcctctttt gtttgataga aaatcataaa aggatttgca 5640
 gactacgggc ctaaagaact aaaaaatcta tctgtttctt ttcattctct gtatttttta 5700
 tagtttctgt tgcacgggca taaagttgcc tttttaatca caattcagaa aatatcataa 5760
 tatctcattt cactaaataa tagtgaacgg caggtatatg tgatgggtta aaaaggatcg 5820
 gcggccgctc gatttaaata tcgagaggcc tgacgtcggg 5860

<210> 70

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 70

cggcaccacc gacatcatct tcacctgcc tcgttccg

38

<210> 71

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 71

cggaacgagg gcaggtgaag atgatgtcgg tgggtgccg

38

<210> 72

<211> 1266

<212> DNA

<213> LysC mutant

<220>

<221> CDS

<222> (1) .. (1266)

<400> 72

gtg gcc ctg gtc gta cag aaa tat ggc ggt tcc tcg ctt gag agt gcg
Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

48

gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

96

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

144

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg 50 55 60	192
gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu 65 70 75 80	240
gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr 85 90 95	288
ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg 100 105 110	336
att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly 115 120 125	384
aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg 130 135 140	432
gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala 145 150 155 160	480
ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val 165 170 175	528
gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys 180 185 190	576
ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly 195 200 205	624
tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn 210 215 220	672
gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu 225 230 235 240	720
att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr 245 250 255	768
ggc gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile 260 265 270	816
tcc gat aag cca ggc gag gct gcg aag gtt ttc cgt gcg ttg gct gat Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp 275 280 285	864

gca gaa atc aac att gac atg gtt ctg cag aac gtc tct tct gta gaa 912
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300

gac ggc acc acc gac atc atc ttc acc tgc cct cgt tcc gac ggc cgc 960
 Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320

cgc gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc 1008
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335

aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct 1056
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350

ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg 1104
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365

cgc gat gtc aac gtg aac atc gaa ttg att tcc acc tct gag att cgt 1152
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380

att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca 1200
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400

ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat 1248
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415

gca ggc acc gga cgc taa 1266
 Ala Gly Thr Gly Arg
 420

<210> 73

<211> 421

<212> PRT

<213> LysC mutant

<400> 73

Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
 1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
 20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 74

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 74

```

cccgggtacca cgcgtcccag tggctgagac gcatccgcta aagccccagg aaccctgtgc      60
agaaagaaaa cactcctctg gctaggtaga cacagtttat aaaggtagag ttgagcgggt      120
aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg      180
cggttcctcg cttgagagtg cggaacgcat tagaaacgtc gctgaacgga tcgttgccac      240

```

caagaaggct ggaaatgatg tcgtggttgt ctgctccgca atgggagaca ccacggatga	300
acttctagaa cttgcagcgg cagtgaatcc cgttccgcca gctcgtgaaa tggatatgct	360
cctgactgct ggtgagcgta tttctaacgc tctcgtcgcc atggctattg agtcccttgg	420
cgcagaagcc caatctttca cgggctctca ggctgggtgtg ctcaccaccg agcgccacgg	480
aaacgcacgc attgttgatg tcaactccagg tcgtgtgcgt gaagcactcg atgagggcaa	540
gatctgcatt gttgctgggt tccaggggtgt taataaagaa acccgcgatg tcaccacgtt	600
gggtcgtggg ggttctgaca ccaactgcagt tgcgttggca gctgctttga acgctgatgt	660
gtgtgagatt tactcggacg ttgacgggtgt gtataccgct gacccgcgca tcgttcctaa	720
tgcacagaag ctggaaaagc tcagcttcga agaaatgctg gaacttgctg ctggttgctc	780
caagattttg gtgctgcgca gtgttgaata cgctcgtgca ttcaatgtgc cacttcgcgt	840
acgctcgtct tatagtaatg atccccggcac tttgattgcc ggctctatgg aggatattcc	900
tgtggaagaa gcagtcctta ccggtgtcgc aaccgacaag tccgaagcca aagtaaccgt	960
tctgggtatt tccgataagc caggcgaggc tgcgaagggt ttccgtgcgt tggctgatgc	1020
agaaatcaac attgacatgg ttctgcagaa cgtctcttct gtagaagacg gcaccaccga	1080
catcatcttc acctgccttc gttccgacgg ccgcccgcgc atggagatct tgaagaagct	1140
tcaggttcag ggcaactgga ccaatgtgct ttacgacgac caggtcggca aagtctccct	1200
cgtgggtgct ggcataaggt ctcaccacgg tgttaccgca gagttcatgg aagctctgcg	1260
cgatgtcaac gtgaacatcg aattgatctc cacctctgag attcgtatct ccgtgctgat	1320
ccgtgaagat gatctggatg ctgctgcacg tgcattgcat gagcagttcc agctgggcgg	1380
cgaagacgaa gccgtcgttt atgcaggcac cggacgctaa agttttaaag gagtagtttt	1440
acaatgacca ccatcgcagt tggttggtgca accggccagg tcggccagggt tatgcgcacc	1500
cttttggaag agcgcaattt cccagctgac actgttcggt tctttgcttc cccacgttcc	1560
gcaggccgta agattgaatt cgtcgacatc gatgctcttc tgcgttaatt aacaattggg	1620
atcctctaga cccgggattt aaatcgctag cgggctgcta aaggaagcgg aacacgtaga	1680
aagccagtcc gcagaaacgg tgctgacccc ggatgaatgt cagctactgg gctatctgga	1740
caagggaaaa cgcaagcgca aagagaaagc aggtagcttg cagtgggctt acatggcgat	1800
agctagactg ggcggtttta tggacagcaa gcgaaccgga attgccagct ggggcgcctt	1860
ctggtaagggt tgggaagccc tgcaaagtaa actggatggc tttcttgccg ccaaggatct	1920
gatggcgcag gggatcaaga tctgatcaag agacaggatg aggatcgttt cgcattgattg	1980
aacaagatgg attgcacgca ggttctccgg ccgcttgggt ggagaggcta ttccgctatg	2040

actgggcaca	acagacaatc	ggctgctctg	atgccgccgt	gttccggctg	tcagcgcagg	2100
ggcgcccgg	tctttttgtc	aagaccgacc	tgtccgggtg	cctgaatgaa	ctgcaggacg	2160
aggcagcgcg	gctatcgtgg	ctggccacga	cgggcgttcc	ttgcgcagct	gtgctcgacg	2220
ttgtcactga	agcgggaagg	gactggctgc	tattggggcg	agtgccgggg	caggatctcc	2280
tgtcatctca	ccttgctcct	gccgagaaa	tatccatcat	ggctgatgca	atgcggcggc	2340
tgcatacgt	tgatccggct	acctgccc	tcgaccacca	agcgaacat	cgcacgcagc	2400
gagcacgtac	tcggatggaa	gccggctctg	tcgatcagga	tgatctggac	gaagagcatc	2460
aggggctcgc	gccagccgaa	ctgttcgcca	ggctcaaggc	gcgcacgccc	gacggcgagg	2520
atctcgtcgt	gacccatggc	gatgcctgct	tgccgaatat	catggtggaa	aatggccgct	2580
tttctggatt	catcgactgt	ggccggctgg	gtgtggcgga	ccgctatcag	gacatagcgt	2640
tggctacccg	tgatattgct	gaagagcttg	gcggcgaatg	ggctgaccgc	ttcctcgtgc	2700
tttacgggtat	cgccgctccc	gattcgcagc	gcacgcctt	ctatcgccct	cttgacgagt	2760
tcttctgagc	gggactctgg	ggttcgaaat	gaccgaccaa	gcgacgccc	acctgccatc	2820
acgagatttc	gattccaccg	ccgccttcta	tgaaagggtg	ggcttcggaa	tcgttttccg	2880
ggacgccggc	tggatgatcc	tccagcgcgg	ggatctcatg	ctggagttct	tcgcccacgc	2940
tagcggcgcg	ccggccggcc	cgggtgtgaa	taccgcacag	atgcgtaagg	agaaaatacc	3000
gcacagggcg	ctcttccgct	tcctcgtc	ctgactcgt	gcgctcggtc	gttcggctgc	3060
ggcgagcgg	atcagctcac	tcaaaggcgg	taatacgggt	atccacagaa	tcaggggata	3120
acgcaggaaa	gaacatgtga	gcaaaaggcc	agcaaaaggc	caggaaccgt	aaaaaggccg	3180
cgttgctggc	gtttttccat	aggctccgcc	cccctgacga	gcacacaaa	aatcgacgct	3240
caagtcagag	gtggcgaaac	ccgacaggac	tataaagata	ccaggcggtt	ccccctggaa	3300
gctccctcgt	gcgctctcct	gttcgacccc	tgccgcttac	cggataacct	tcgccttttc	3360
tccttccggg	aagcgtggcg	ctttctcata	gtcacgctg	taggtatctc	agttcgggtg	3420
aggctcgttcg	ctccaagctg	ggctgtgtgc	acgaaccccc	cgttcagccc	gaccgctgcg	3480
ccttatccgg	taactatcgt	cttgagtcca	accggttaag	acacgactta	tcgccactgg	3540
cagcagccac	tggtaacagg	attagcagag	cagaggtatg	aggcgggtgt	acagagttct	3600
tgaagtgggtg	gcctaactac	ggctacacta	gaaggacagt	atttggtatc	tcgctctgc	3660
tgaagccagt	taccttcgga	aaaagagttg	gtagctcttg	atccggcaaa	caaaccaccg	3720
ctggtagcgg	tggttttttt	gtttgcaagc	agcagattac	gcgcagaaaa	aaaggatctc	3780
aagaagatcc	tttgatcttt	tctacggggg	ctgacgctca	gtggaacgaa	aactcacggt	3840

aagggatttt	ggtcatgaga	ttatcaaaaa	ggatcttcac	ctagatcctt	ttaaaggccg	3900
gccgcggccg	ccatcggcat	tttcttttgc	gtttttat	gttaactg	aattgtcctt	3960
gttcaaggat	gctgtctttg	acaacagatg	tttctttgcc	tttgatgttc	agcaggaagc	4020
tcggcgcaaa	cgttgattgt	ttgtctgcgt	agaatcctct	gtttgtcata	tagcttgtaa	4080
tcacgacatt	gtttcctttc	gcttgaggta	cagcgaagtg	tgagtaagta	aaggttacat	4140
cgttaggatc	aagatccatt	tttaacacaa	ggccagtttt	gttcagcggc	ttgtatgggc	4200
cagttaaaga	attagaaaca	taaccaagca	tgtaaata	gttagacgta	atgccgtcaa	4260
tcgtcatttt	tgatccgcgg	gagtcagtga	acaggtagca	tttgccgttc	attttaaaga	4320
cgttcgcg	ttcaatttca	tctgttactg	tgtagatgc	aatcagcgg	ttcatcactt	4380
ttttcagtgt	gtaatcatcg	tttagctcaa	tcataccgag	agcgcggtt	gctaactcag	4440
ccgtgcgttt	tttatcgctt	tgcaagaagt	ttgactttc	ttgacggaag	aatgatgtgc	4500
ttttgccata	gtatgctttg	ttaaataaag	attcttcgcc	ttggtagcca	tcttcagttc	4560
cagtgtttgc	ttcaaatact	aagtatttgt	ggcctttatc	ttctacgtag	tgaggatctc	4620
tcagcgtatg	gttgctgcct	gagctgtagt	tgccctcatc	gatgaactgc	tgtacatttt	4680
gatacgtttt	tccgtcaccg	tcaaagattg	atttataatc	ctctacaccg	ttgatgttca	4740
aagagctgtc	tgatgctgat	acgttaactt	gtgcagttgt	cagtgtttgt	ttgccgtaat	4800
gtttaccgga	gaaatcagtg	tagaataaac	ggatttttcc	gtcagatgta	aatgtggctg	4860
aacctgacca	ttcttgtgtt	tggcttttta	ggatagaatc	atttgcatcg	aatttgtcgc	4920
tgtctttaaa	gacgcggcca	gcgtttttcc	agctgtcaat	agaagtttcg	ccgacttttt	4980
gatagaacat	gtaaatcgat	gtgtcatccg	catttttagg	atctccggct	aatgcaaaga	5040
cgatgtggta	gccgtgatag	tttgcgacag	tgccgtcagc	gttttgtaat	ggccagctgt	5100
cccaaacgtc	caggcctttt	gcagaagaga	tattttta	tgtggacgaa	tcaaattcag	5160
aaacttgata	tttttcattt	ttttgctgtt	cagggatttg	cagcatatca	tggcgtgtaa	5220
tatgggaaat	gccgtatgtt	tccttatatg	gcttttggtt	cgtttctttc	gcaaacgctt	5280
gagttgcgcc	tcctgccagc	agtgcggtag	taaagggttaa	tactgttgct	tgttttgcaa	5340
actttttgat	gttcatcggt	catgtctcct	tttttatgta	ctgtgttagc	ggctctgctt	5400
ttccagccct	cctgtttgaa	gatggcaagt	tagttacgca	caataaaaaa	agacctaaaa	5460
tatgtaaggg	gtgacgcaa	agtatacact	ttgcccttta	cacatttttag	gtcttgccctg	5520
ctttatcagt	aacaaaccg	cgcgatttac	ttttcgacct	cattctatta	gactctcggt	5580
tggattgcaa	ctgggtctatt	ttcctctttt	gtttgataga	aaatcataaa	aggatttgca	5640

gactacgggc ctaaagaact aaaaaatcta tctgtttctt ttcattctct gtatttttta 5700
tagtttctgt tgcattgggca taaagttgcc tttttaatca caattcagaa aatatcataa 5760
tatctcattt cactaaataa tagtgaacgg caggtatatg tgatgggtta aaaaggatcg 5820
gcggccgctc gatttaaata tcgagaggcc tgacgtcggg 5860

<210> 75

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 75

gagactcgag gtagacttta aacccatatt ag

32

<210> 76

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR primer

<400> 76

gaagtctaga ttagcgaata gcgtcgtgg

29

<210> 77

<211> 6142

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 77

tcgaggtaga ctttaaacc atattagagg gtgggggcgc agctaagcca agagctaaga

60

aaactagggg acatagtgg atcgacgtg ttcaataacg gcaacctaca gtaaaaatga

120

ataaaattcc tcaaggtggc aatattcttc aattttccca taaaatacgc ccgtatgtct	180
gcacaaccgc tacctgctgc gtatcagcgc acaatcaccg atgtcatttc catgccaaaca	240
ccgggccagg ttccgttttc tgtagagttt atgccgccac gagatgagggc agcagaagag	300
cgactctgga aagccgccga agcatttcac gacttaggag cctcttttgt ctccgttact	360
tatggtgcag gcggatctag ccgcgagcgc acaatgcgtg tcgcgcacaa gctttctcgt	420
catccgttga ccacgctcgt tcatctcacg cttgtggaac acaccaaga agaattagaa	480
gaaattctgt gcacttatgc gtcccacggg ttgtctaact tacttgcctt gcgagggcat	540
ccccctggca ctgaccgat ggctccgtgg gtccctaccg caggcggcct agattatgcc	600
aaagatttga tcgacctcgt gcgcaagact gagcagacct cgcactttca ggtaggaatt	660
gctagtttcc cagaagggca ctaccgagcg cctagcattg aggcggatac gcaatttaca	720
ttggaaaagc tgcgagctgg cgcagagttt tcgattacc cagatgtttt tgatgtcgat	780
cactatttac gactgcgaga tcgcttggtt aaggcggatc ctgaacatgg atcaaagccg	840
atcatcccag gacttatgcc cattaccagc ttgaggtcgg ttcgtaggca gatggaatta	900
gcaggtgcc a cttgcctaa ggcttttagaa aaacggcttc tcgacgcagc gcgcggcgat	960
gaggaagctc atcgcggcga tattcgcaaa gtaggaatcg aagtcactac tgagatggca	1020
cagcgtctta tttctgaagg gatcccagac atccatttca tgaccatgaa ttatgttcga	1080
gcgaccaag aagtactcca taatctcggc atggcgcccg cgtggggaac acagcaaggc	1140
cacgacgcta ttcgctaate tagaccggg atttaaatec ctagcgggct gctaaaggaa	1200
gcggaacacg tagaaagcca gtccgcagaa acgggtgctga ccccgatga atgtcagcta	1260
ctgggctatc tggacaaggg aaaacgcaag cgcaaagaga aagcaggtag cttgcagtgg	1320
gcttacatgg cgatagctag actgggcggg tttatggaca gcaagcgaac cggaattgcc	1380
agctggggcg ccctctggta aggttgggaa gccctgcaaa gttaaactgga tggctttctt	1440
gccgccaaag atctgatggc gcaggggatc aagatctgat caagagacag gatgaggatc	1500
gtttcgcattg attgaacaag atggattgca cgcaggttct ccggccgctt gggaggagag	1560
gctattcggc tatgactggg cacaacagac aatcggctgc totgatgccg ccgtgttccg	1620
gctgtcagcg caggggccc cggttctttt tgtcaagacc gacctgtccg gtgccctgaa	1680
tgaactgcag gacgaggcag cgcggctatc gtggctggcc acgacgggcg ttccttgccg	1740
agctgtgctc gacgttgtca ctgaagcggg aagggaactgg ctgctattgg gcgaagtgcc	1800
ggggcaggat ctctgtcat ctacacttgc tctgcccag aaagtatcca tcatggctga	1860
tgcaatgcgg cggctgcata cgcttgatcc ggctacctgc ccattcgacc accaagcgaa	1920

acatcgcatc gagcgagcac gtactcggat ggaagccggt cttgtcgatc aggatgatct	1980
ggacgaagag catcaggggc tcgcgccagc cgaactgttc gccagggtca aggcgcgcat	2040
gcccgcggc gaggatctcg tcgtgaccca tggcgatgcc tgcttgccga atatcatggt	2100
ggaaaatggc cgcttttctg gattcatcga ctgtggccgg ctgggtgtgg cggaccgcta	2160
tcaggacata gcgttggcta cccgtgatat tgctgaagag cttggcggcg aatgggctga	2220
ccgcttcctc gtgctttacg gtatcgccgc tcccgattcg cagcgcatcg ccttctatcg	2280
ccttcttgac gagttcttct gagcgggact ctggggttcg aaatgaccga ccaagcgacg	2340
cccaacctgc catcacgaga tttcgattcc accgcgcct tctatgaaag gttgggcttc	2400
ggaatcgttt tccgggacgc cggctggatg atcctccagc gcggggatct catgctggag	2460
ttcttcgccc acgctagcgg cgcgcgggcc ggcccgggtg gaaataccgc acagatgcgt	2520
aaggagaaaa taccgcatca ggcgctcttc cgcttcctcg ctactgact cgctgcgctc	2580
ggtcgttcgg ctgcggcgag cggtatcagc tcaactcaaag gcggtaatac ggttatccac	2640
agaatcaggg gataacgcag gaaagaacat gtgagcaaaa ggccagcaaa aggccaggaa	2700
ccgtaaaaag gccgcgttgc tggcgttttt ccataggctc cgccccctg acgagcatca	2760
caaaaatcga cgctcaagtc agagggtggcg aaacccgaca ggactataaa gataccaggc	2820
gtttccccct ggaagctccc tcgtgcgctc tcctgttccg accctgccgc ttaccggata	2880
cctgtccgcc tttctccctt cgggaagcgt ggcgctttct catagctcac gctgtaggta	2940
tctcagttcg gtgtaggtcg ttcgctccaa gctgggctgt gtgcacgaac cccccgttca	3000
gcccgcaccg tcgcgccttat ccggtaacta tcgtcttgag tocaaccgcg taagacacga	3060
cttatcgcca ctggcagcag ccactggtaa caggattagc agagcgaggt atgtaggcgg	3120
tgctacagag ttcttgaagt ggtggcctaa ctacggctac actagaagga cagtatttgg	3180
tatctgcgct ctgctgaagc cagttacctt cggaaaaaga gttggtagct cttgatccgg	3240
caaacaaacc accgctggta gcggtggttt ttttgtttgc aagcagcaga ttacgcgcag	3300
aaaaaaagga tctcaagaag atcctttgat cttttctacg gggctctgacg ctcagtggaa	3360
cgaaaactca cgttaaggga ttttggtcac gagattatca aaaaggatct tcacctagat	3420
ccttttaaag gccggccgcg gccgcgcaaa gtcccgttc gtgaaaattt tcgtgccgcg	3480
tgattttccg ccaaaaactt taacgaacgt tcgttataat ggtgtcatga ctttcacgac	3540
gaagtactaa aattggcccg aatcatcagc tatggatctc tctgatgtcg cgctggagtc	3600
cgacgcgctc gatgctgccg tcgatttaaa aacggtgacg ggatttttcc gagctctcga	3660
tacgacggac gcgccagcat cacgagactg ggccagtgcc gcgagcgacc tagaaactct	3720

cgtggcggat	cttgaggagc	tggctgacga	gctgcgtgct	cggccagcgc	caggaggacg	3780
cacagtagtg	gaggatgcaa	tcagttgcgc	ctactgcggt	ggcctgattc	ctccccggcc	3840
tgacccgcga	ggacggcgcg	caaaatattg	ctcagatgcg	tgtcgtgccg	cagccagccg	3900
cgagcgcgcc	aacaaacgcc	acgccgagga	gctggaggcg	gctaggtcgc	aaatggcgct	3960
ggaagtgcgt	cccccgagcg	aaattttggc	catggtcgtc	acagagctgg	aagcggcagc	4020
gagaattatc	gcgatcgtgg	cggtgccccgc	aggcatgaca	aacatcgtaa	atgccgcgtt	4080
tcgtgtgccg	tggccgcccc	ggacgtgtca	gcgccgccac	cacctgcacc	gaatcggcag	4140
cagcgtcgcg	cgtcgaaaaa	gcgcacaggc	ggcaagaagc	gataagctgc	acgaatacct	4200
gaaaaatggt	gaacgccccg	tgagcggtaa	ctcacagggc	gtcggctaac	ccccagtcca	4260
aacctgggag	aaagcgcctc	aaaatgactc	tagcggattc	acgagacatt	gacacaccgg	4320
cctggaaatt	ttccgctgat	ctgttcgaca	cccatccccg	gctcgcgctg	cgatcacgtg	4380
gctggacgag	cgaagaccgc	cgcgaattcc	tcgtcacct	gggcagagaa	aatttccagg	4440
gcagcaagac	ccgcgacttc	gccagcgctt	ggatcaaaga	cccggacacg	gagaaacaca	4500
gccgaagtta	taccgagttg	gttcaaaatc	gcttgcccgg	tgccagtatg	ttgctctgac	4560
gcacgcgcag	cacgcagccg	tgcttgtcct	ggacattgat	gtgccgagcc	accaggccgg	4620
cgggaaaatc	gagcacgtaa	accccgaggt	ctacgcgatt	ttggagcgct	gggcacgcct	4680
ggaaaaagcg	ccagcttgga	tggcgctgaa	tccactgagc	gggaaatgcc	agctcatctg	4740
gctcattgat	ccggtgtatg	ccgcagcagg	catgagcagc	ccgaatatgc	gcctgctggc	4800
tgcaacgacc	gaggaaatga	cccgcgtttt	cggcgctgac	caggcttttt	cacataggct	4860
gagccgtggc	cactgcactc	tccgacgata	ccagccgtac	cgtgggcatg	cccagcacia	4920
tcgcgtggat	cgcttagctg	atcttatgga	ggttgctcgc	atgatctcag	gcacagaaaa	4980
acctaataaaa	cgctatgagc	aggagttttc	tagcggacgg	gcacgtatcg	aagcggcaag	5040
aaaagccact	gcggaagcaa	aagcacttgc	cacgcttgaa	gcaagcctgc	cgagcgccgc	5100
tgaagcgtct	ggagagctga	tcgacggcgt	ccgtgtcctc	tggactgctc	cagggcgctgc	5160
cgcccgatgat	gagacggcct	ttcgccacgc	tttgactgtg	ggataccagt	taaaagcggc	5220
tggtgagcgc	ctaaaagaca	ccaagggcta	tcgagcctac	gagcgtgcct	acaccgtcgc	5280
tcaggcggtc	ggaggaggcc	gtgagcctga	tctgccgccg	gactgtgacc	gccagacgga	5340
ttggccgcga	cgtgtgcgcg	gctacgtcgc	taaaggccag	ccagtcgtcc	ctgctcgtca	5400
gacagagacg	cagagccagc	cgaggcgaaa	agctctggcc	actatgggaa	gacgtggcgg	5460
taaaaaggcc	gcagaacgct	ggaaagaccc	aaacagtgag	tacgcccag	cacagcgaga	5520

aaaactagct aagtccagtc aacgacaagc taggaaagct aaaggaaatc gcttgaccat	5580
tgccaggttg tttatgactg ttgagggaga gactggctcg tggccgacaa tcaatgaagc	5640
tatgtctgaa tttagcgtgt cacgtcagac cgtgaataga gcacttaagg tctgcgggca	5700
ttgaacttcc acgaggacgc cgaaagcttc ccagtaaagt tgccatctcg taggcagaaa	5760
acggttcccc cgtagggctc ctctcttggc ctcttttcta ggtagggctg attgctcttg	5820
aagctctcta ggggggctca caccataggc agataacgtt cccaccggc tcgcctcgta	5880
agcgcacaag gactgctccc aaagatcttc aaagccactg ccgcgactgc cttcgcgaa	5940
ccttgccccg cggaaatttc ctccaccgag ttcgtgcaca cccctatgcc aagcttcttt	6000
caccctaaat tcgagagatt ggattcttac cgtggaaatt cttcgcaaaa atcgtcccct	6060
gatcgccctt gcgacgttg cgtaggtgcc gctgggtgcg cttggcttga ccgacttgat	6120
cagcgccgc tcgatttaaa tc	6142